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(30) Priority Data:		(71) Applicant (for all designated States except US): ARENA PHARMACEUTICALS, INC. [US/US]; 6166 Nancy Ridge Drive, San Diego, CA 92121 (US).	
60/109,213	20 November 1998 (20.11.98) US	(72) Inventors; and	
60/120,416	16 February 1999 (16.02.99) US	(75) Inventors/Applicants (for US only): CHEN, Ruoping [CN/US];	
60/121,852	26 February 1999 (26.02.99) US	5296 Timber Branch Way, San Diego, CA 92130 (US).	
60/123,946	12 March 1999 (12.03.99) US	DANG, Huong, T. [US/US]; 5352 Oak Park Drive, San	
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60/136,437	28 May 1999 (28.05.99) US	8291-7 Gold Coast Drive, San Diego, CA 92126 (US).	
60/136,439	28 May 1999 (28.05.99) US	(74) Agents: MILLER, Suzanne, E. et al.; Woodcock Washburn	
60/136,567	28 May 1999 (28.05.99) US	Kurtz Mackiewicz & Norris LLP, 46th floor, One Liberty	
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(54) Title: HUMAN ORPHAN G PROTEIN-COUPLED RECEPTORS			
(57) Abstract			
The invention disclosed in this patent document relates to transmembrane receptors, more particularly to endogenous, human orphan G protein-coupled receptors.			

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HUMAN ORPHAN G PROTEIN-COUPLED RECEPTORS

This patent document claims priority benefit of each of the following applications, all filed with the United States Patent and Trademark Office via U.S. Express Mail on the indicated filing dates: U.S. Provisional Number 60/121,852, filed; February 26, 1999 claiming the benefit of U.S. Provisional Number 60/109,213, filed November 20, 1998; U.S. Provisional Number 60/120,416, filed February 16, 1999; U.S. Provisional Number 60/123,946, filed March 12, 1999; U.S. Provisional Number 60/123,949, filed March 12, 1999; U.S. Provisional Number 60/136,436, filed May 28, 1999; U.S. Provisional Number 60/136,439, filed May 28, 1999; U.S. Provisional Number 60/136,567, filed May 28, 1999; U.S. Provisional Number 60/137,127, filed May 28, 1999; U.S. Provisional Number 60/137,131, filed May 28, 1999; U.S. Provisional Number 141,448, filed June 29, 1999 claiming priority from U.S. Provisional Number 60/136,437, filed May 28, 1999; U.S. Provisional Number _____ (Arena Pharmaceuticals, Inc. docket number CHN10-1), filed September 29, 1999; U.S. Provisional Number 60/156,333, filed September 29, 1999; U.S. Provisional Number 60/156,555, filed September 29, 1999; U.S. Provisional Number 60/156,634, filed September 29, 1999; U.S. Provisional Number _____ (Arena Pharmaceuticals, Inc. docket number RUP6-1), filed October 1, 1999; U.S. Provisional Number _____ (Arena Pharmaceuticals, Inc. docket number RUP7-1), filed October 1, 1999; U.S. Provisional Number _____ (Arena Pharmaceuticals, Inc. docket number CHN6-1), filed October 1, 1999; U.S. Provisional

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Number _____ (Arena Pharmaceuticals, Inc. docket number RUP5-1), filed October 1, 1999; U.S. Provisional Number _____ (Arena Pharmaceuticals, Inc. docket number CHN9-1), filed October 1, 1999. This patent document is related to U.S. Serial Number 09/170,496 filed October 13, 1998, and U.S. Serial Number unknown (Woodcock
5 Washburn Kurtz Mackiewicz & Norris, LLP docket number AREN-0054) filed on October 12, 1999 (via U.S. Express Mail) both being incorporated herein by reference. This patent document also is related to U.S. Serial No. 09/364,425; filed July 30, 1999, which is incorporated by reference in its entirety. This application also claims priority to U.S. Serial Number _____ (Woodcock, Washburn, Kurtz, Makiewicz & Norris, LLP
10 docket number AREN-0050), filed on October 12, 1999 (via U.S. Express Mail), incorporated by reference herein in its entirety. Each of the foregoing applications are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

The invention disclosed in this patent document relates to transmembrane receptors,
15 and more particularly to endogenous, orphan, human G protein-coupled receptors ("GPCRs").

BACKGROUND OF THE INVENTION

Although a number of receptor classes exist in humans, by far the most abundant and therapeutically relevant is represented by the G protein-coupled receptor (GPCR or GPCRs)
20 class. It is estimated that there are some 100,000 genes within the human genome, and of these, approximately 2% or 2,000 genes, are estimated to code for GPCRs. Receptors, including GPCRs, for which the endogenous ligand has been identified are referred to as "known" receptors, while receptors for which the endogenous ligand has not been identified

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are referred to as "orphan" receptors. GPCRs represent an important area for the development of pharmaceutical products: from approximately 20 of the 100 known GPCRs, 60% of all prescription pharmaceuticals have been developed. This distinction is not merely semantic, particularly in the case of GPCRs. Thus, the orphan GPCRs are to the pharmaceutical industry what gold was to California in the late 19th century – an opportunity to drive growth, expansion, enhancement and development.

GPCRs share a common structural motif. All these receptors have seven sequences of between 22 to 24 hydrophobic amino acids that form seven alpha helices, each of which spans the membrane (each span is identified by number, *i.e.*, transmembrane-1 (TM-1), transmembrane-2 (TM-2), etc.). The transmembrane helices are joined by strands of amino acids between transmembrane-2 and transmembrane-3, transmembrane-4 and transmembrane-5, and transmembrane-6 and transmembrane-7 on the exterior, or "extracellular" side, of the cell membrane (these are referred to as "extracellular" regions 1, 2 and 3 (EC-1, EC-2 and EC-3), respectively). The transmembrane helices are also joined by strands of amino acids between transmembrane-1 and transmembrane-2, transmembrane-3 and transmembrane-4, and transmembrane-5 and transmembrane-6 on the interior, or "intracellular" side, of the cell membrane (these are referred to as "intracellular" regions 1, 2 and 3 (IC-1, IC-2 and IC-3), respectively). The "carboxy" ("C") terminus of the receptor lies in the intracellular space within the cell, and the "amino" ("N") terminus of the receptor lies in the extracellular space outside of the cell.

Generally, when an endogenous ligand binds with the receptor (often referred to as "activation" of the receptor), there is a change in the conformation of the intracellular region that allows for coupling between the intracellular region and an intracellular "G-protein." It

has been reported that GPCRs are "promiscuous" with respect to G proteins, *i.e.*, that a GPCR can interact with more than one G protein. *See*, Kenakin, T., 43 *Life Sciences* 1095 (1988). Although other G proteins exist, currently, Gq, Gs, Gi, and Go are G proteins that have been identified. Endogenous ligand-activated GPCR coupling with the G-protein begins a signaling cascade process (referred to as "signal transduction"). Under normal conditions, signal transduction ultimately results in cellular activation or cellular inhibition. It is thought that the IC-3 loop as well as the carboxy terminus of the receptor interact with the G protein.

Under physiological conditions, GPCRs exist in the cell membrane in equilibrium between two different conformations: an "inactive" state and an "active" state. A receptor in an inactive state is unable to link to the intracellular signaling transduction pathway to produce a biological response. Changing the receptor conformation to the active state allows linkage to the transduction pathway (via the G-protein) and produces a biological response. A receptor may be stabilized in an active state by an endogenous ligand or a compound such as a drug.

SUMMARY OF THE INVENTION

Disclosed herein are human endogenous orphan G protein-coupled receptors.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B provide reference "grids" for certain dot-blots provided herein (see also, Figure 2A and 2B, respectively).

Figures 2A and 2B provide reproductions of the results of certain dot-blot analyses resulting from hCHN3 and hCHN8, respectively (see also, Figures 1A and 1B, respectively).

Figure 3 provides a reproduction of the results of RT-PCR analysis of hRUP3.

Figure 4 provides a reproduction of the results of RT-PCR analysis of hRUP4.

Figure 5 provides a reproduction of the results of RT-PCR analysis of hRUP6.

DETAILED DESCRIPTION

The scientific literature that has evolved around receptors has adopted a number of terms to refer to ligands having various effects on receptors. For clarity and consistency, the following definitions will be used throughout this patent document. To the extent that these definitions conflict with other definitions for these terms, the following definitions shall control:

AMINO ACID ABBREVIATIONS used herein are set out in Table 1:

10	TABLE 1		
	ALANINE	ALA	A
	ARGININE	ARG	R
	ASPARAGINE	ASN	N
	ASPARTIC ACID	ASP	D
15	CYSTEINE	CYS	C
	GLUTAMIC ACID	GLU	E
	GLUTAMINE	GLN	Q
	GLYCINE	GLY	G
	HISTIDINE	HIS	H
20	ISOLEUCINE	ILE	I
	LEUCINE	LEU	L
	LYSINE	LYS	K
	METHIONINE	MET	M
	PHENYLALANINE	PHE	F
25	PROLINE	PRO	P
	SERINE	SER	S
	THREONINE	THR	T
	TRYPTOPHAN	TRP	W
	TYROSINE	TYR	Y
30	VALINE	VAL	V

COMPOSITION means a material comprising at least one component.

ENDOGENOUS shall mean a material that a mammal naturally produces.

ENDOGENOUS in reference to, for example and not limitation, the term "receptor," shall mean that which is naturally produced by a mammal (for example, and not limitation, a

human) or a virus. By contrast, the term **NON-ENDOGENOUS** in this context shall mean that which is not naturally produced by a mammal (for example, and not limitation, a human) or a virus.

HOST CELL shall mean a cell capable of having a Plasmid and/or Vector incorporated therein. In the case of a prokaryotic Host Cell, a Plasmid is typically replicated as a autonomous molecule as the Host Cell replicates (generally, the Plasmid is thereafter isolated for introduction into a eukaryotic Host Cell); in the case of a eukaryotic Host Cell, a Plasmid is integrated into the cellular DNA of the Host Cell such that when the eukaryotic Host Cell replicates, the Plasmid replicates. Preferably, for the purposes of the invention disclosed herein, the Host Cell is eukaryotic, more preferably, mammalian, and most preferably selected from the group consisting of 293, 293T and COS-7 cells.

LIGAND shall mean an endogenous, naturally occurring molecule specific for an endogenous, naturally occurring receptor.

NON-ORPHAN RECEPTOR shall mean an endogenous naturally occurring molecule specific for an endogenous naturally occurring ligand wherein the binding of a ligand to a receptor activates an intracellular signaling pathway.

ORPHAN RECEPTOR shall mean an endogenous receptor for which the endogenous ligand specific for that receptor has not been identified or is not known.

PLASMID shall mean the combination of a Vector and cDNA. Generally, a Plasmid is introduced into a Host Cell for the purposes of replication and/or expression of the cDNA as a protein.

VECTOR in reference to cDNA shall mean a circular DNA capable of incorporating at least one cDNA and capable of incorporation into a Host Cell.

The order of the following sections is set forth for presentational efficiency and is not intended, nor should be construed, as a limitation on the disclosure or the claims to follow.

Identification of Human GPCRs

5 The efforts of the Human Genome project have led to the identification of a plethora of information regarding nucleic acid sequences located within the human genome; it has been the case in this endeavor that genetic sequence information has been made available without an understanding or recognition as to whether or not any particular genomic sequence does or may contain open-reading frame information that translate human proteins.

10 Several methods of identifying nucleic acid sequences within the human genome are within the purview of those having ordinary skill in the art. For example, and not limitation, a variety of GPCRs, disclosed herein, were discovered by reviewing the GenBank™ database, while other GPCRs were discovered by utilizing a nucleic acid sequence of a GPCR, previously sequenced, to conduct a BLAST™ search of the EST database. **Table A**, below,

15 lists the disclosed endogenous orphan GPCRs along with a GPCR's respective homologous GPCR:

TABLE A

	Disclosed	Accession	Open Reading	Per Cent	Reference To
	Human	Number	Frame	Homology	Homologous
20	Orphan	Identified	(Base Pairs)	To Designated	GPCR
	GPCRs			GPCR	(Accession No.)
	hARE-3	AL033379	1,260 bp	52.3% LPA-R	U92642
	hARE-4	AC006087	1,119 bp	36% P2Y5	AF000546

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	hARE-5	AC006255	1,104 bp	32% <i>Oryzias</i>	D43633
				<i>latipes</i>	
	hGPR27	AA775870	1,128 bp		
	hARE-1	AI090920	999 bp	43%	D13626
				KIAA0001	
	hARE-2	AA359504	1,122 bp	53% GPR27	
5	hPPR1	H67224	1,053 bp	39% EBI1	L31581
	hG2A	AA754702	1,113 bp	31% GPR4	L36148
	hRUP3	AL035423	1,005 bp	30%	2133653
				<i>Drosophila</i>	
				<i>melanogaster</i>	
	hRUP4	AI307658	1,296 bp	32% pNPGPR	NP_004876
				28% and 29 %	AAC41276
				<i>Zebra fish</i> Ya	and
				and Yb,	AAB94616
				respectively	
	hRUP5	AC005849	1,413 bp	25% DEZ	Q99788
				23% FMLPR	P21462
10	hRUP6	AC005871	1,245 bp	48% GPR66	NP_006047
	hRUP7	AC007922	1,173 bp	43% H3R	AF140538
	hCHN3	EST 36581	1,113 bp	53% GPR27	
	hCHN4	AA804531	1,077 bp	32% thrombin	4503637
	hCHN6	EST 2134670	1,503 bp	36% edg-1	NP_001391
15	hCHN8	EST 764455	1,029 bp	47%	D13626
				KIAA0001	
	hCHN9	EST 1541536	1,077 bp	41% LTB4R	NM_000752
	hCHN10	EST 1365839	1,055 bp	35% P2Y	NM_002563

Receptor homology is useful in terms of gaining an appreciation of a role of the disclosed receptors within the human body. Additionally, such homology can provide insight as to possible endogenous ligand(s) that may be natural activators for the disclosed orphan GPCRs.

B. Receptor Screening

Techniques have become more readily available over the past few years for

endogenous-ligand identification (this, primarily, for the purpose of providing a means of conducting receptor-binding assays that require a receptor's endogenous ligand) because the traditional study of receptors has always proceeded from the a priori assumption (historically based) that the endogenous ligand must first be identified before discovery could proceed to find antagonists and other molecules that could affect the receptor. Even in cases where an antagonist might have been known first, the search immediately extended to looking for the endogenous ligand. This mode of thinking has persisted in receptor research even after the discovery of constitutively activated receptors. What has not been heretofore recognized is that it is the active state of the receptor that is most useful for discovering agonists, partial agonists, and inverse agonists of the receptor. For those diseases which result from an overly active receptor or an under-active receptor, what is desired in a therapeutic drug is a compound which acts to diminish the active state of a receptor or enhance the activity of the receptor, respectively, not necessarily a drug which is an antagonist to the endogenous ligand. This is because a compound that reduces or enhances the activity of the active receptor state need not bind at the same site as the endogenous ligand. Thus, as taught by a method of this invention, any search for therapeutic compounds should start by screening compounds against the ligand-independent active state.

As is known in the art, GPCRs can be "active" in their endogenous state even without the binding of the receptor's endogenous ligand thereto. Such naturally-active receptors can be screened for the direct identification (*i.e.*, without the need for the receptor's endogenous ligand) of, in particular, inverse agonists. Alternatively, the receptor can be "activated" via, *e.g.*, mutation of the receptor to establish a non-endogenous version of the receptor that is active in the absence of the receptor's endogenous ligand.

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Screening candidate compounds against an endogenous or non-endogenous, constitutively activated version of the human orphan GPCRs disclosed herein can provide for the direct identification of candidate compounds which act at this cell surface receptor, without requiring use of the receptor's endogenous ligand. By determining areas within the body where the endogenous version of human GPCRs disclosed herein is expressed and/or over-expressed, it is possible to determine related disease/disorder states which are associated with the expression and/or over-expression of the receptor; such an approach is disclosed in this patent document.

With respect to creation of a mutation that may evidence constitutive activation of human orphan GPCRs disclosed herein is based upon the distance from the proline residue at which is presumed to be located within TM6 of the GPCR typically nears the TM6/IC3 interface (such proline residue appears to be quite conserved). By mutating the amino acid residue located 16 amino acid residues from this residue (presumably located in the IC3 region of the receptor) to, most preferably, a lysine residue, such activation may be obtained. Other amino acid residues may be useful in the mutation at this position to achieve this objective.

C. Disease/Disorder Identification and/or Selection

Preferably, the DNA sequence of the human orphan GPCR can be used to make a probe for (a) dot-blot analysis against tissue-mRNA, and/or (b) RT-PCR identification of the expression of the receptor in tissue samples. The presence of a receptor in a tissue source, or a diseased tissue, or the presence of the receptor at elevated concentrations in diseased tissue compared to a normal tissue, can be preferably utilized to identify a correlation with a treatment regimen, including but not limited to, a disease associated

with that disease. Receptors can equally well be localized to regions of organs by this technique. Based on the known functions of the specific tissues to which the receptor is localized, the putative functional role of the receptor can be deduced.

D. Screening of Candidate Compounds

5 1. Generic GPCR screening assay techniques

When a G protein receptor becomes constitutively active (i.e., active in the absence of endogenous ligand binding thereto), it binds to a G protein (*e.g.*, Gq, Gs, Gi, Go) and stimulates the binding of GTP to the G protein. The G protein then acts as a GTPase and slowly hydrolyzes the GTP to GDP, whereby the receptor, under normal conditions, becomes
10 deactivated. However, constitutively activated receptors continue to exchange GDP to GTP.

A non-hydrolyzable analog of GTP, [³⁵S]GTPγS, can be used to monitor enhanced binding to membranes which express constitutively activated receptors. It is reported that [³⁵S]GTPγS can be used to monitor G protein coupling to membranes in the absence and presence of ligand. An example of this monitoring, among other examples well-known and
15 available to those in the art, was reported by Traynor and Nahorski in 1995. The preferred use of this assay system is for initial screening of candidate compounds because the system is generically applicable to all G protein-coupled receptors regardless of the particular G protein that interacts with the intracellular domain of the receptor.

2. Specific GPCR screening assay techniques

20 Once candidate compounds are identified using the "generic" G protein-coupled receptor assay (*i.e.*, an assay to select compounds that are agonists, partial agonists, or inverse agonists), further screening to confirm that the compounds have interacted at the receptor site is preferred. For example, a compound identified by the "generic" assay may not bind to the

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receptor, but may instead merely "uncouple" the G protein from the intracellular domain.

a. Gs and Gi.

Gs stimulates the enzyme adenylyl cyclase. Gi (and Go), on the other hand, inhibit this enzyme. Adenylyl cyclase catalyzes the conversion of ATP to cAMP; thus, constitutively activated GPCRs that couple the Gs protein are associated with increased cellular levels of cAMP. On the other hand, constitutively activated GPCRs that couple the Gi (or Go) protein are associated with decreased cellular levels of cAMP. *See, generally, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992).* Thus, assays that detect cAMP can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to the receptor (*i.e.*, such a compound would decrease the levels of cAMP). A variety of approaches known in the art for measuring cAMP can be utilized; a most preferred approach relies upon the use of anti-cAMP antibodies in an ELISA-based format. Another type of assay that can be utilized is a whole cell second messenger reporter system assay. Promoters on genes drive the expression of the proteins that a particular gene encodes. Cyclic AMP drives gene expression by promoting the binding of a cAMP-responsive DNA binding protein or transcription factor (CREB) which then binds to the promoter at specific sites called cAMP response elements and drives the expression of the gene. Reporter systems can be constructed which have a promoter containing multiple cAMP response elements before the reporter gene, *e.g.*, β -galactosidase or luciferase. Thus, a constitutively activated Gs-linked receptor causes the accumulation of cAMP that then activates the gene and expression of the reporter protein. The reporter protein such as β -galactosidase or luciferase can then be detected using standard biochemical assays (Chen et al. 1995).

Go and Gq.

Gq and Go are associated with activation of the enzyme phospholipase C, which in turn hydrolyzes the phospholipid PIP_2 , releasing two intracellular messengers: 5 diacylglycerol (DAG) and inistol 1,4,5-triphoisphate (IP_3). Increased accumulation of IP_3 is associated with activation of Gq- and Go-associated receptors. *See, generally*, "Indirect Mechanisms of Synaptic Transmission," Chpt. 8, From Neuron To Brain (3rd Ed.) Nichols, J.G. et al eds. Sinauer Associates, Inc. (1992). Assays that detect IP_3 accumulation can be utilized to determine if a candidate compound is, *e.g.*, an inverse agonist to a Gq- or Go- 10 associated receptor (*i.e.*, such a compound would decrease the levels of IP_3). Gq-associated receptors can also been examined using an AP1 reporter assay in that Gq-dependent phospholipase C causes activation of genes containing AP1 elements; thus, activated Gq-associated receptors will evidence an increase in the expression of such genes, whereby inverse agonists thereto will evidence a decrease in such expression, and agonists will 15 evidence an increase in such expression. Commercially available assays for such detection are available.

3. GPCR Fusion Protein

The use of an endogenous, constitutively activated orphan GPCR, or a non-endogenous, constitutively activated orphan GPCR, for screening of candidate compounds 20 for the direct identification of inverse agonists, agonists and partial agonists provides a unique challenge in that, by definition, the receptor is active even in the absence of an endogenous ligand bound thereto. Thus, it is often useful that an approach be utilized that can enhance the signal obtained by the activated receptor. A preferred approach is the use of a GPCR Fusion Protein.

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Generally, once it is determined that a GPCR is or has been constitutively activated, using the assay techniques set forth above (as well as others), it is possible to determine the predominant G protein that couples with the endogenous GPCR. Coupling of the G protein to the GPCR provides a signaling pathway that can be assessed. Because it is most preferred that screening take place by use of a mammalian expression system, such a system will be expected to have endogenous G protein therein. Thus, by definition, in such a system, the constitutively activated orphan GPCR will continuously signal. In this regard, it is preferred that this signal be enhanced such that in the presence of, *e.g.*, an inverse agonist to the receptor, it is more likely that it will be able to more readily differentiate, particularly in the context of screening, between the receptor when it is contacted with the inverse agonist.

The GPCR Fusion Protein is intended to enhance the efficacy of G protein coupling with the GPCR. The GPCR Fusion Protein is preferred for screening with a non-endogenous, constitutively activated GPCR because such an approach increases the signal that is most preferably utilized in such screening techniques, although the GPCR Fusion Protein can also be (and preferably is) used with an endogenous, constitutively activated GPCR. This is important in facilitating a significant "signal to noise" ratio; such a significant ratio is important preferred for the screening of candidate compounds as disclosed herein.

The construction of a construct useful for expression of a GPCR Fusion Protein is within the purview of those having ordinary skill in the art. Commercially available expression vectors and systems offer a variety of approaches that can fit the particular needs of an investigator. The criteria of importance for such a GPCR Fusion Protein construct is that the GPCR sequence and the G protein sequence both be in-frame (preferably, the sequence for the GPCR is upstream of the G protein sequence) and that the "stop" codon of

the GPCR must be deleted or replaced such that upon expression of the GPCR, the G protein can also be expressed. The GPCR can be linked directly to the G protein, or there can be spacer residues between the two (preferably, no more than about 12, although this number can be readily ascertained by one of ordinary skill in the art). We have a preference (based upon convenience) of use of a spacer in that some restriction sites that are not used will, effectively, upon expression, become a spacer. Most preferably, the G protein that couples to the GPCR will have been identified prior to the creation of the GPCR Fusion Protein construct. Because there are only a few G proteins that have been identified, it is preferred that a construct comprising the sequence of the G protein (*i.e.*, a universal G protein construct) be available for insertion of an endogenous GPCR sequence therein; this provides for efficiency in the context of large-scale screening of a variety of different endogenous GPCRs having different sequences.

E. Other Utility

Although a preferred use of the human orphan GPCRs disclosed herein may be for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists (preferably for use as pharmaceutical agents), these versions of human GPCRs can also be utilized in research settings. For example, *in vitro* and *in vivo* systems incorporating GPCRs can be utilized to further elucidate and understand the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signaling cascade. The value in human orphan GPCRs is that its utility as a research tool is enhanced in that by determining the location(s) of such receptors within the body, the GPCRs can be used to understand the role of these receptors in the human body before the endogenous ligand therefor is identified.

Other uses of the disclosed receptors will become apparent to those in the art based upon, *inter alia*, a review of this patent document.

EXAMPLES

The following examples are presented for purposes of elucidation, and not limitation, of the present invention. While specific nucleic acid and amino acid sequences are disclosed herein, those of ordinary skill in the art are credited with the ability to make minor modifications to these sequences while achieving the same or substantially similar results reported below. Unless otherwise indicated below, all nucleic acid sequences for the disclosed endogenous orphan human GPCRs have been sequenced and verified. For purposes of equivalent receptors, those of ordinary skill in the art will readily appreciate that conservative substitutions can be made to the disclosed sequences to obtain a functionally equivalent receptor.

Example 1

ENDOGENOUS HUMAN GPCRS

1. Identification of Human GPCRs

Several of the disclosed endogenous human GPCRs were identified based upon a review of the GenBank database information. While searching the database, the following cDNA clones were identified as evidenced below.

Disclosed	Accession	Complete DNA	Open Reading	Nucleic Acid	Amino
Human	Number	Sequence	Frame	SEQ.ID.	Acid
Orphan		(Base Pairs)	(Base Pairs)	NO.	SEQ.ID.
GPCRs					NO.

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	hARE-3	AL033379	111,389 bp	1,260 bp	1	2
	hARE-4	AC006087	226,925 bp	1,119 bp	3	4
	hARE-5	AC006255	127,605 bp	1,104 bp	5	6
	hRUP3	AL035423	140,094 bp	1,005 bp	7	8
5	hRUP5	AC005849	169,144 bp	1,413 bp	9	10
	hRUP6	AC005871	218,807 bp	1,245 bp	11	12
	hRUP7	AC007922	158,858 bp	1,173 bp	13	14

Other disclosed endogenous human GPCRs were identified by conducting a BLAST search of EST database (dbest) using the following EST clones as query sequences. The 10 following EST clones identified were then used as a probe to screen a human genomic library.

	Disclosed	Query	EST Clone/	Open	Nucleic Acid	Amino Acid
	Human	(Sequence)	Accession No.	Reading	SEQ.ID.NO.	SEQ.ID.NO.
	Orphan		Identified	Frame		
15	GPCRs			(Base Pairs)		
	hGPCR27	Mouse	AA775870	1,125 bp	15	16
	hARE-1	GPCR27 TDAG	1689643	999 bp	17	18
	hARE-2	GPCR27	AI090920 68530	1,122 bp	19	20
	hPPR1	Bovine	AA359504 238667	1,053 bp	21	22
20	hG2A	PPR1 Mouse	H67224 <i>See Example 2(a),</i>	1,113 bp	23	24
		1179426	<i>below</i>			

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	hCHN3	N.A.	EST 36581	1,113 bp	25	26
	hCHN4	TDAG	(full length) 1184934	1,077 bp	27	28
	hCHN6	N.A.	AA804531 EST 2134670	1,503 bp	29	30
	hCHN8	KIAA0001	(full length) EST 764455	1,029 bp	31	32
5	hCHN 9	1365839	EST 1541536	1,077 bp	33	34
	hCHN10	Mouse EST	Human 1365839	1,005 bp	35	36
	hRUP4	1365839 N.A.	AI307658	1,296 bp	37	38

N.A. = "not applicable".

2. Full Length Cloning

10 a. hG2A (Seq. Id. Nos. 23 & 24)

Mouse EST clone 1179426 was used to obtain a human genomic clone containing all but three amino acid hG2A coding sequences. The 5' end of this coding sequence was obtained by using 5'RACE™, and the template for PCR was Clontech's Human Spleen Marathon-ready™ cDNA. The disclosed human G2A was amplified by PCR using the G2A
15 cDNA specific primers for the first and second round PCR as shown in SEQ.ID.NO.: 39 and SEQ.ID.NO.:40 as follows:

5'-CTGTGTACAGCAGTTCGCAGAGTG-3' (SEQ.ID.NO.: 39; 1st round PCR)

5'-GAGTGCCAGGCAGAGCAGGTAGAC-3' (SEQ.ID.NO.: 40; second round PCR).

PCR was performed using Advantage™ GC Polymerase Kit (Clontech; manufacturing
20 instructions will be followed), at 94°C for 30 sec followed by 5 cycles of 94°C for 5 sec and 72°C for 4 min; and 30 cycles of 94° for 5 sec and 70° for 4 min. An approximate 1.3 Kb PCR fragment was purified from agarose gel, digested with Hind III and Xba I and cloned into the expression vector pRC/CMV2 (Invitrogen). The cloned-insert was sequenced using the T7 Sequenase™ kit (USB Amersham; manufacturer instructions will be followed) and

the sequence was compared with the presented sequence. Expression of the human G2A will be detected by probing an RNA dot blot (Clontech; manufacturer instructions will be followed) with the P³²-labeled fragment.

b. hCHN9 (Seq. Id. Nos. 33 & 34)

5 Sequencing of the EST clone 1541536 indicated that hCHN9 is a partial cDNA clone having only an initiation codon; *i.e.*, the termination codon was missing. When hCHN9 was used to "blast" against the data base (nr), the 3' sequence of hCHN9 was 100% homologous to the 5' untranslated region of the leukotriene B4 receptor cDNA, which contained a termination codon in the frame with hCHN9 coding sequence. To
10 determine whether the 5' untranslated region of LTB4R cDNA was the 3' sequence of hCHN9, PCR was performed using primers based upon the 5' sequence flanking the initiation codon found in hCHN9 and the 3' sequence around the termination codon found in the LTB4R 5' untranslated region. The 5' primer sequence utilized was as follows:

5'-CCCGAATTCCTGCTTGCTCCCAGCTTGGCCC-3' (SEQ.ID.NO.: 41; sense) and

15 5'-TGTGGATCCTGCTGTCAAAGGTCCCATTCGGG-3' (SEQ.ID.NO.: 42; antisense).

PCR was performed using thymus cDNA as a template and rTth polymerase (Perkin Elmer) with the buffer system provided by the manufacturer, 0.25 uM of each primer, and 0.2 mM of each 4 nucleotides. The cycle condition was 30 cycles of 94°C for 1 min, 65°C for 1 min and 72 °C for 1 min and 10 sec. A 1.1kb fragment consistent with the predicted size was
20 obtained from PCR. This PCR fragment was subcloned into pCMV (*see below*) and sequenced (*see*, SEQ.ID.NO.: 33).

c. hRUP 4 (Seq. Id. Nos. 37 & 38)

The full length hRUP4 was cloned by RT-PCR with human brain cDNA (Clontech)

as templates:

5'-TCACAATGCTAGGTGTGGTC-3' (SEQ.ID.NO.: 43; sense) and

5'-TGCATAGACAATGGGATTACAG-3' (SEQ.ID.NO.: 44; antisense).

PCR was performed using TaqPlus™ Precision™ polymerase (Stratagene; manufacturing instructions will be followed) by the following cycles: 94°C for 2 min; 94°C 30 sec; 55°C for 30 sec, 72°C for 45 sec, and 72°C for 10 min. Cycles 2 through 4 were repeated 30 times.

The PCR products were separated on a 1% agarose gel and a 500 bp PCR fragment was isolated and cloned into the pCRII-TOPO vector (Invitrogen) and sequenced using the 10 T7 DNA Sequenase™ kit (Amsham) and the SP6/T7 primers (Stratagene). Sequence analysis revealed that the PCR fragment was indeed an alternatively spliced form of AI307658 having a continuous open reading frame with similarity to other GPCRs. The completed sequence of this PCR fragment was as follows:

```

5'-TCACAATGCTAGGTGTGGTCTGGCTGGTGGCAGTCATCGTAGGATCACCCATGTGGCAC
15 GTGCAACAACCTGAGATCAAATATGACTTCCTATATGAAAAGGAACACATCTGCTGCTTAGAA
   GAGTGGACCAGCCCTGTGCACCAGAAGATCTACACCACCTTCATCCTTGTCATCCTCTTCCTCC
   TGCCTCTTATGGTGATGCTTATTCTGTACGTAAATTTGGTTATGAACTTTGGATAAAGAAAAGA
   GTTGGGGATGGTTCAGTGCTTCGAACTATTCATGGAAAAGAAATGTCCAAAATAGCCAGGAAG
   AAGAAACGAGCTGTCATTATGATGGTGACAGTGGTGGCTCTCTTTGCTGTGTGCTGGGCACCA
20 TTCCATGTTGTCCATATGATGATTGAATACAGTAATTTTGAAAAGGAATATGATGATGTCACA
   ATCAAGATGATTTTGTCTATCGTGCAAATTATTGGATTTTCCAACCTCCATCTGTAATCCCATTG
   TCTATGCA-3' (SEQ.ID.NO.: 45)

```

Based on the above sequence, two sense oligonucleotide primer sets:

5'-CTGCTTAGAAGAGTGGACCAG-3' (SEQ.ID.NO.: 46; oligo 1),

25 5'-CTGTGCACCAGAAGATCTACAC-3' (SEQ.ID.NO.: 47; oligo 2)

and two antisense oligonucleotide primer sets:

5'-CAAGGATGAAGGTGGTGTAGA-3' (SEQ.ID.NO.: 48; oligo 3)

5'-GTGTAGATCTTCTGGTGCACAGG-3' (SEQ.ID.NO.: 49; oligo 4)

were used for 3'- and 5'-race PCR with a human brain Marathon-Ready™ cDNA (Clontech,

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Cat# 7400-1) as template, according to manufacture's instructions. DNA fragments generated by the RACE PCR were cloned into the pCRII-TOPO™ vector (Invitrogen) and sequenced using the SP6/T7 primers (Stratagene) and some internal primers. The 3' RACE product contained a poly(A) tail and a completed open reading frame ending at a TAA stop codon. The 5' RACE product contained an incomplete 5' end; *i.e.*, the ATG initiation codon was not present.

Based on the new 5' sequence, oligo 3 and the following primer:

5'-GCAATGCAGGTCATAGTGAGC -3' (SEQ.ID.NO.: 50; oligo 5)

were used for the second round of 5' RACE PCR and the PCR products were analyzed as above. A third round of 5' RACE PCR was carried out utilizing antisense primers:

5'-TGGAGCATGGTGACGGGAATGCAGAAG-3' (SEQ.ID.NO.: 51; oligo 6) and

5'-GTGATGAGCAGGTCACTGAGCGCCAAG-3' (SEQ.ID.NO.: 52; oligo 7).

The sequence of the 5' RACE PCR products revealed the presence of the initiation codon ATG, and further round of 5' RACE PCR did not generate any more 5' sequence. The completed 5' sequence was confirmed by RT-PCR using sense primer

5'-GCAATGCAGGCGCTTAACATTAC-3' (SEQ.ID.NO.: 53; oligo 8)

and oligo 4 as primers and sequence analysis of the 650 bp PCR product generated from human brain and heart cDNA templates (Clontech, Cat# 7404-1). The completed 3' sequence was confirmed by RT-PCR using oligo 2 and the following antisense primer:

5'-TTGGGTTACAATCTGAAGGGCA-3' (SEQ.ID.NO.: 54; oligo 9)

and sequence analysis of the 670 bp PCR product generated from human brain and heart cDNA templates. (Clontech, Cat# 7404-1).

d. hRUP5 (Seq. Id. Nos. 9 & 10)

The full length hRUP5 was cloned by RT-PCR using a sense primer upstream from

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ATG, the initiation codon (SEQ.ID.NO.: 55), and an antisense primer containing TCA as the stop codon (SEQ.ID.NO.: 56), which had the following sequences:

5'-ACTCCGTGTCCAGCAGGACTCTG-3' (SEQ.ID.NO.:55)

5'-TGC GTG TTCCTGGACCCTCACGTG-3' (SEQ.ID.NO.: 56)

5 and human peripheral leukocyte cDNA (Clontech) as a template. Advantage cDNA polymerase (Clontech) was used for the amplification in a 50ul reaction by the following cycle with step 2 through step 4 repeated 30 times: 94°C for 30 sec; 94° for 15 sec; 69° for 40 sec; 72°C for 3 min; and 72°C fro 6 min. A 1.4kb PCR fragment was isolated and cloned with the pCRII-TOPO™ vector (Invitrogen) and completely sequenced using the T7 DNA 10 Sequenase™ kit (Amsham). See, SEQ.ID.NO.: 9.

e. hRUP6 (Seq. Id. Nos. 11 & 12)

The full length hRUP6 was cloned by RT-PCR using primers:

5'-CAGGCCTTGGATTTTAATGTCAGGGATGG-3' (SEQ.ID.NO.: 57) and

5'-GGAGAGTCAGCTCTGAAAGAATTCAGG-3' (SEQ.ID.NO.: 58);

15 and human thymus Marathon-Ready™ cDNA (Clontech) as a template. Advantage cDNA polymerase (Clontech, according to manufacturer's instructions) was used for the amplification in a 50ul reaction by the following cycle: 94°C for 30sec; 94°C for 5 sec; 66°C for 40sec; 72°C for 2.5 sec and 72°C for 7 min. Cycles 2 through 4 were repeated 30 times. A 1.3 Kb PCR fragment was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) 20 and completely sequenced (see, SEQ.ID.NO.: 11) using the ABI Big Dye Terminator™ kit (P.E. Biosystem).

f. hRUP7 (Seq. Id. Nos. 13 & 14)

The full length RUP7 was cloned by RT-PCR using primers:

5'-TGATGTGATGCCAGATACTAATAGCAC-3' (SEQ.ID.NO.: 59; sense) and

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5'-CCTGATTCATTTAGGTGAGATTGAGAC-3' (SEQ.ID.NO.: 60; antisense) and human peripheral leukocyte cDNA (Clontech) as a template. Advantage™ cDNA polymerase (Clontech) was used for the amplification in a 50 ul reaction by the following cycle with step 2 to step 4 repeated 30 times: 94°C for 2 minutes; 94°C for 15 seconds; 60°C for 20 seconds; 72°C for 2 minutes; 72°C for 10 minutes. A 1.25 Kb PCR fragment was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced using the ABI Big Dye Terminator™ kit (P.E. Biosystem). See, SEQ.ID.NO.: 13.

g. hARE-5 (Seq. Id. Nos. 5 & 6)

The full length hARE-5 was cloned by PCR using the hARE5 specific primers 10 5'-CAGCGCAGGGTGAAGCCTGAGAGC-3' SEQ.ID.NO.: 69 (sense, 5' of initiation codon ATG) and 5'-GGCACCTGCTGTGACCTGTGCAGG-3' SEQ.ID.NO.:70 (antisense, 3' of stop codon TGA) and human genomic DNA as template. TaqPlus Precision™ DNA polymerase (Stratagene) was used for the amplification by the following cycle with step 2 to step 4 repeated 35 times: 96°C, 2 minutes; 96°C, 20 seconds; 58°C, 30 seconds; 72°C, 2 minutes; and 72°C, 10 minutes

15 A 1.1 Kb PCR fragment of predicated size was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced (SEQ.ID.NO.:5) using the T7 DNA Sequenase™ kit (Amsham).

h. hARE-4 (Seq. Id. Nos.: 3 & 4)

The full length hARE-4 was cloned by PCR using the hARE-4 specific primers 5'-20 CTGGTGTGCTCCATGGCATCCC-3' SEQ.ID.NO.:67 (sense, 5' of initiation codon ATG) and 5'-GTAAGCCTCCCAGAACGAGAGG-3' SEQ.ID.NO.: 68 (antisense, 3' of stop codon TGA) and human genomic DNA as template. Taq DNA polymerase (Stratagene) and 5% DMSO was used for the amplification by the following cycle with step 2 to step 3 repeated 35 times:

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94°C, 3 minutes; 94°C, 30 seconds; 59°C, 2 minutes; 72°C, 10 minutes

A 1.12 Kb PCR fragment of predicated size was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced (SEQ.ID.NO.:3) using the T7 DNA Sequenase™ kit (Amsham).

5 **i. hARE-3 (Seq.Id.Nos.: 1 & 2)**

The full length hARE-3 was cloned by PCR using the hARE-3 specific primers 5'-gatcaagcttCCATCCTACTGAAACCATGGTC-3' SEQ.ID.NO.:65 (sense, lower case nucleotides represent Hind III overhang, ATG as initiation codon) and 5'-gatcagatctCAGTTCCAATATTCACACCACCGTC-3' SEQ.ID.NO.:66 (antisense, lower case 10 nucleotides represent Xba I overhang, TCA as stop codon) and human genomic DNA as template. TaqPlus Precision™ DNA polymerase (Stratagene) was used for the amplification by the following cycle with step 2 to step 4 repeated 35 times: 94°C, 3 minutes; 94°C, 1 minute; 55°C, 1 minute; 72°C, 2 minutes; 72°C, 10 minutes.

A 1.3 Kb PCR fragment of predicated size was isolated and digested with Hind III 15 and Xba I, cloned into the pRC/CMV2 vector (Invitrogen) at the Hind III and Xba I sites and completely sequenced (SEQ.ID.NO.:1) using the T7 DNA Sequenase™ kit (Amsham).

j. hRUP3 (Seq. Id. Nos.:7 & 8)

The full length hRUP3 was cloned by PCR using the hRUP3 specific primers 5'-GTCCTGCCACTTCGAGACATGG-3' SEQ.ID.NO.:71 (sense, ATG as initiation codon) and 5'-20 GAAACTTCTCTGCCCTTACCGTC-3' SEQ.ID.NO.:72 (antisense, 3' of stop codon TAA) and human genomic DNA as template. TaqPlus Precision™ DNA polymerase (Stratagene) was used for the amplification by the following cycle with step 2 to step 4 repeated 35 times: 94°C, 3 minutes; 94°C, 1 minute; 58°C, 1 minute; 72°C, 2 minutes; 72°C, 10 minutes

A 1.0 Kb PCR fragment of predicated size was isolated and cloned into the pCRII-TOPO™ vector (Invitrogen) and completely sequenced (SEQ.ID.NO.: 7) using the T7 DNA sequenase kit (Amsham).

Example 2

5 RECEPTOR EXPRESSION

Although a variety of cells are available to the art for the expression of proteins, it is most preferred that mammalian cells be utilized. The primary reason for this is predicated upon practicalities, *i.e.*, utilization of, *e.g.*, yeast cells for the expression of a GPCR, while possible, introduces into the protocol a non-mammalian cell which may not (indeed, in the case of yeast, does not) include the receptor-coupling, genetic-mechanism and secretory pathways that have evolved for mammalian systems – thus, results obtained in non-mammalian cells, while of potential use, are not as preferred as that obtained from mammalian cells. Of the mammalian cells, COS-7, 293 and 293T cells are particularly preferred, although the specific mammalian cell utilized can be predicated upon the particular needs of the artisan. The general procedure for expression of the disclosed GPCRs is as follows.

On day one, 1×10^7 293T cells per 150mm plate were plated out. On day two, two reaction tubes will be prepared (the proportions to follow for each tube are per plate): tube A will be prepared by mixing 20µg DNA (*e.g.*, pCMV vector; pCMV vector with receptor cDNA, etc.) in 1.2ml serum free DMEM (Irvine Scientific, Irvine, CA); tube B will be prepared by mixing 120µl lipofectamine (Gibco BRL) in 1.2ml serum free DMEM. Tubes A and B are admixed by inversions (several times), followed by incubation at room temperature for 30-45min. The admixture can be referred to as the "transfection mixture". Plated 293T cells are washed with 1XPBS, followed by addition of 10ml serum free DMEM.

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2.4ml of the transfection mixture will then be added to the cells, followed by incubation for 4hrs at 37°C/5% CO₂. The transfection mixture was then be removed by aspiration, followed by the addition of 25ml of DMEM/10% Fetal Bovine Serum. Cells will then be incubated at 37°C/5% CO₂. After 72hr incubation, cells can then be harvested and utilized for analysis.

5 Example 3

TISSUE DISTRIBUTION OF THE DISCLOSED HUMAN GPCRS

Several approaches can be used for determination of the tissue distribution of the GPCRs disclosed herein.

1. Dot-Blot Analysis

10 Using a commercially available human-tissue dot-blot format, endogenous orphan GPCRs were probed for a determination of the areas where such receptors are localized. cDNA fragments from the GPCRs of Example 1 (radiolabelled) were (or can be) used as the probe: radiolabeled probe was (or can be) generated using the complete receptor cDNA (excised from the vector) using a Prime-It II™ Random Primer Labeling Kit (Stratagene, 15 #300385), according to manufacturer's instructions. A human RNA Master Blot™ (Clontech, #7770-1) was hybridized with the endogenous human GPCR radiolabeled probe and washed under stringent conditions according manufacturcr's instructions. The blot was exposed to Kodak BioMax™ Autoradiography film overnight at -80°C. Results are summarized for several receptors in Table B and C (see Figures 1A and 1B for a grid 20 identifying the various tissues and their locations, respectively). Exemplary dot-blot results are provided in Figure 2A and 2B for results derived using hCHN3 and hCHN8, respectively.

TABLE B

ORPHAN GPCR

Tissue Distribution
(highest levels, relative to other tissues in the dot-blot)

- 27 -

	hGPCR27	Fetal brain, Putamen, Pituitary gland, Caudate nucleus
	hARE-1	Spleen, Peripheral leukocytes, Fetal spleen
	hPPR1	Pituitary gland, Heart, salivary gland, Small intestine, Testis
	hRUP3	Pancreas
5	hCHN3	Fetal brain, Putamen, Occipital cortex
	hCHN9	Pancreas, Small intestine, Liver
	hCHN10	Kidney, Thryoid

TABLE C

	ORPHAN GPCR	Tissue Distribution (highest levels, relative to other tissues in the dot-blot)
10	hARE-3	Cerebellum left, Cerebellum right, Testis, Accumbens
	hGPCR3	Corpus collusum, Caudate nucleus, Liver, Heart, Inter-Ventricular Septum
	hARE-2	Cerebellum left, Cerebellum right, Substantia
	hCHN8	Cerebellum left, Cerebellum right, Kidney, Lung

2. RT-PCR

15 a. hRUP3

To ascertain the tissue distribution of hRUP3 mRNA, RT-PCR was performed using hRUP3-specific primers and human multiple tissue cDNA panels (MTC, Clontech) as templates. Taq DNA polymerase (Stratagene) was utilized for the PCR reaction, using the following reaction cycles in a 40ul reaction: 94°C for 2 min; 94°C for 15 sec; 55°C for 30 sec; 72°C for 1 min; 72°C, for 10 min. Primers were as follows:

5'-GACAGGTACCTTGCCATCAAG-3' (SEQ.ID.NO.: 61; sense)

5'-CTGCACAATGCCAGTGATAAGG-3' (SEQ.ID.NO.: 62; antisense).

20ul of the reaction was loaded onto a 1% agarose gel; results are set forth in Figure 3.

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As is supported by the data of Figure 3, of the 16 human tissues in the cDNA panel utilized (brain, colon, heart, kidney, lung, ovary, pancreas, placenta, prostate, skeleton, small intestine, spleen, testis, thymus leukocyte, and liver) a single hRUP3 band is evident only from the pancreas. Additional comparative analysis of the protein sequence of hRUP3 with 5 other GPCRs suggest that hRUP3 is related to GPCRs having small molecule endogenous ligand such that it is predicted that the endogenous ligand for hRUP3 is a small molecule.

b. hRUP4

RT-PCR was performed using hRUP4 oligo's 8 and 4 as primers and the human multiple tissue cDNA panels (MTC, Clontech) as templates. Taq DNA polymerase 10 (Stratagene) was used for the amplification in a 40ul reaction by the following cycles: 94°C for 30 seconds, 94°C for 10 seconds, 55°C for 30 seconds, 72°C for 2 minutes, and 72°C for 5 minutes with cycles 2 through 4 repeated 30 times.

20 µl of the reaction were loaded on a 1% agarose gel to analyze the RT-PCR products, and hRUP4 mRNA was found expressed in many human tissues, with the strongest 15 expression in heart and kidney. (*see*, Figure 4). To confirm the authenticity of the PCR fragments, a 300 bp fragment derived from the 5' end of hRUP4 was used as a probe for the Southern Blot analysis. The probe was labeled with ³²P-dCTP using the Prime-It II™ Random Primer Labeling Kit (Stratagene) and purified using the ProbeQuant™ G-50 micro columns (Amersham). Hybridization was done overnight at 42° C following a 12 hr pre-20 hybridization. The blot was finally washed at 65°C with 0.1 x SSC. The Southern blot did confirm the PCR fragments as hRUP4.

c. hRUP5

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RT-PCR was performed using the following hRUP5 specific primers:

5'-CTGACTTCTTGTTCTGTCCTGGCAGCAGCGG-3' (SEQ.ID.NO.: 63; sense)

5'-AGACCAGCCAGGGCACGCTGAAGAGTG-3' (SEQ.ID.NO.: 64; antisense)

and the human multiple tissue cDNA panels (MTC, Clontech) as templates. Taq DNA polymerase (Stratagene) was used for the amplification in a 40ul reaction by the following cycles: 94°C for 30 sec, 94°C for 10 sec, 62°C for 1.5 min, 72°C for 5 min, and with cycles 2 through 3 repeated 30 times. 20 µl of the reaction were loaded on a 1.5% agarose gel to analyze the RT-PCR products, and hRUP5 mRNA was found expressed only in the peripheral blood leukocytes (*data not shown*).

10 **d. hRUP6**

RT-PCR was applied to confirm the expression and to determine the tissue distribution of hRUP6. Oligonucleotides used, based on an alignment of AC005871 and GPR66 segments, had the following sequences:

5'-CCAACACCAGCATCCATGGCATCAAG-3' (SEQ.ID.NO.: 73; sense),

15 5'-GGAGAGTCAGCTCTGAAAGAATTCAGG-3' (SEQ.ID.NO.: 74; antisense)

and the human multiple tissue cDNA panels (MTC, Clontech) were used as templates.

PCR was performed using TaqPlus Precision™ polymerase (Stratagene; manufacturing instructions will be followed) in a 40ul reaction by the following cycles: 94°C for 30 sec; 94°C 5 sec; 66°C for 40 sec, 72°C for 2.5 min, and 72°C for 7 min. Cycles 2 through 4
20 were repeated 30 times.

20 ul of the reaction were loaded on a 1.2% agarose gel to analyze the RT-PCR products, and a specific 760bp DNA fragment representing hRUP6 was expressed predominantly in the thymus and with less expression in the heart, kidney, lung, prostate small intestine and testis. (*see*, Figure 5).

It is intended that each of the patents, applications, and printed publications mentioned in this patent document be hereby incorporated by reference in their entirety.

As those skilled in the art will appreciate, numerous changes and modifications may be made to the preferred embodiments of the invention without departing from the spirit of the invention. It is intended that all such variations fall within the scope of the invention and the claims that follow.

Although a variety of Vectors are available to those in the art, for purposes of utilization for both endogenous and non-endogenous human GPCRs, it is most preferred that the Vector utilized be pCMV. This vector was deposited with the American Type Culture Collection (ATCC) on October 13, 1998 (10801 University Blvd., Manassas, VA 20110-2209 USA) under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure. The DNA was tested by the ATCC and determined to be. The ATCC has assigned the following deposit number to pCMV: ATCC #203351.

CLAIMS

What is claimed is:

1. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 1.
- 5 2. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 1 comprising SEQ.ID.NO.: 2.
3. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:1.
4. A Host Cell comprising the Plasmid of claim 3.
5. A cDNA encoding a human G protein-coupled receptor comprising
10 SEQ.ID.NO.: 3.
6. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 3 comprising SEQ.ID.NO.: 4.
7. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:3.
8. A Host Cell comprising the Plasmid of claim 7.
- 15 9. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 5.
10. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 5 comprising SEQ.ID.NO.: 6.
11. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:5.
- 20 12. A Host Cell comprising the Plasmid of claim 11.
13. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 7.

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14. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 7 comprising SEQ.ID.NO.: 8.
15. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:7.
16. A Host Cell comprising the Plasmid of claim 15.
- 5 17. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 9.
18. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 9 comprising SEQ.ID.NO.: 10.
19. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:9.
- 10 20. A Host Cell comprising the Plasmid of claim 19.
21. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 11.
22. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 11 comprising SEQ.ID.NO.:12.
- 15 23. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:11.
24. A Host Cell comprising the Plasmid of claim 23.
25. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 13.
26. A human G protein-coupled receptor encoded by the cDNA of
20 SEQ.ID.NO.: 13 comprising SEQ.ID.NO.: 14.
27. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:13.
28. A Host Cell comprising the Plasmid of claim 27.
29. A cDNA encoding a human G protein-coupled receptor comprising

SEQ.ID.NO.: 15.

30. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 15 comprising SEQ.ID.NO.: 16.

31. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:15.

5 32. A Host Cell comprising the Plasmid of claim 31.

33. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 17.

34. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 17 comprising SEQ.ID.NO.: 18.

10 35. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:17.

36. A Host Cell comprising the Plasmid of claim 35.

37. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 19.

15 38. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 19 comprising SEQ.ID.NO.: 20.

39. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:19.

40. A Host Cell comprising the Plasmid of claim 39.

41. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 21.

20 42. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 21 comprising SEQ.ID.NO.: 22.

43. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:21.

44. A Host Cell comprising the Plasmid of claim 43.

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45. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 23.
46. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 23 comprising SEQ.ID.NO.: 24.
- 5 47. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.: 23.
48. A Host Cell comprising the Plasmid of claim 47.
49. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 25.
50. A human G protein-coupled receptor encoded by the cDNA of
10 SEQ.ID.NO.: 25 comprising SEQ.ID.NO.: 26.
51. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:25.
52. A Host Cell comprising the Plasmid of claim 51.
53. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 27.
- 15 54. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 27 comprising SEQ.ID.NO.: 28.
55. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:27.
56. A Host Cell comprising the Plasmid of claim 55.
57. A cDNA encoding a human G protein-coupled receptor comprising
20 SEQ.ID.NO.: 29.
58. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 29 comprising SEQ.ID.NO.: 30.
59. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:29.

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60. A Host Cell comprising the Plasmid of claim 59.
61. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 31.
62. A human G protein-coupled receptor encoded by the cDNA of
5 SEQ.ID.NO.: 31 comprising SEQ.ID.NO.: 32.
63. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:31.
64. A Host Cell comprising the Plasmid of claim 63.
65. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 33.
- 10 66. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 33 comprising SEQ.ID.NO.: 34.
67. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:33.
68. A Host Cell comprising the Plasmid of claim 67.
69. A cDNA encoding a human G protein-coupled receptor comprising
15 SEQ.ID.NO.: 35.
70. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 35 comprising SEQ.ID.NO.: 36.
71. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:35.
72. A Host Cell comprising the Plasmid of claim 71.
- 20 73. A cDNA encoding a human G protein-coupled receptor comprising
SEQ.ID.NO.: 37.
74. A human G protein-coupled receptor encoded by the cDNA of
SEQ.ID.NO.: 37 comprising SEQ.ID.NO.: 38.

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75. A Plasmid comprising a Vector and the cDNA of SEQ.ID.NO.:37.
76. A Host Cell comprising the Plasmid of claim 75.

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	1	2	3	4	5	6	7	8
A		Amygdala	Caudate Nucleus	Cerebellum	Cerebral Cortex	Frontal Cortex	Hippocampus	Medulla Oblongata
B	Occipital Cortex	Putamen	Substantia Nigra	Temporal Cortex	Thalamus	Accumbens	Spinal Cord	
C	Heart	Aorta	Skeletal Muscle	Colon	Bladder	Uterus	Prostate	Stomach
D	Testis	Ovary	Pancreas	Pituitary	Adrenal Gland	Thyroid	Salivary Gland	Mammary Gland
E	Kidney	Liver	Small Intestine	Spleen	Thymus	Peripheral Leukocyte	Lymph Node	Bone Marrow
F	Appendix	Lung	Trachea	Placenta				
G	Fetal Brain	Fetal Heart	Fetal Kidney	Fetal Liver	Fetal Spleen	Fetal Thymus	Fetal Lung	
H								

FIG. 1A

	1	2	3	4	5	6	7	8	9	10	11	12
A		Cerebellum Left	Substantia Nigra	Heart	Esophagus	Colon Transverse	Kidney	Lung	Liver	Leukemia HL-60	Fetal Brain	
B	Cerebral Cortex	Cerebellum Right	Accumbens	Aorta	Stomach	Colon Descending	Skeletal Muscle	Placenta	Pancreas	HeLa S3	Fetal Heart	
C	Frontal Cortex	Corpus Callosum	Thalamus	Atrium Left	Duodenum	Rectum	Spleen	Bladder	Adrenal Gland	Leukemia K562	Fetal Kidney	
D	Parietal Lobe	Amygdala	Pituitary Gland	Atrium Right	Jejunum		Thymus	Uterus	Thyroid	Leukemia MOLT-4	Fetal Liver	
E	Occipital Cortex	Caudate Nucleus	Spinal Cord	Ventricle Left	Ileum		Peripheral Leukocyte	Prostate	Salivary Gland	Burkitt's Lymphoma Raji	Fetal Spleen	
F	Temporal Cortex	Hippocampus		Ventricle Right	Ileocecum		Lymph Node	Testis	Mammary Gland	Burkitt's Lymphoma Daudi	Fetal Thymus	
G	Paracentral Gyrus of Cerebral Cortex	Medulla Oblongata		Inter Ventricular Septum	Appendix		Bone Marrow	Ovary		Colorectal Adenocarcinoma SW480	Fetal Lung	
H	Pons	Putamen		Apex of the Heart	Colon Ascending		Trachea			Lung Carcinoma A549		

FIG. 1B

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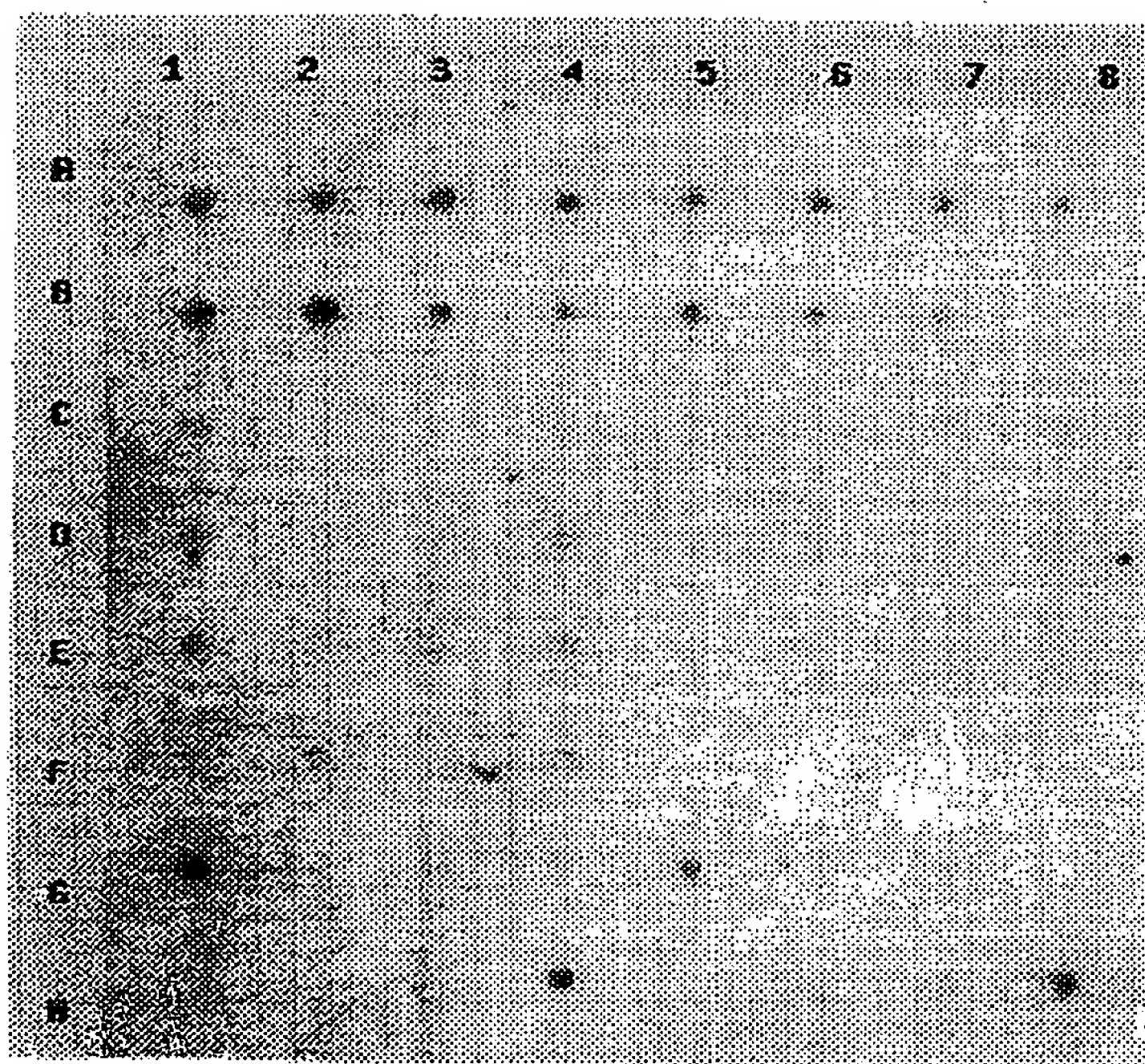


FIG. 2A

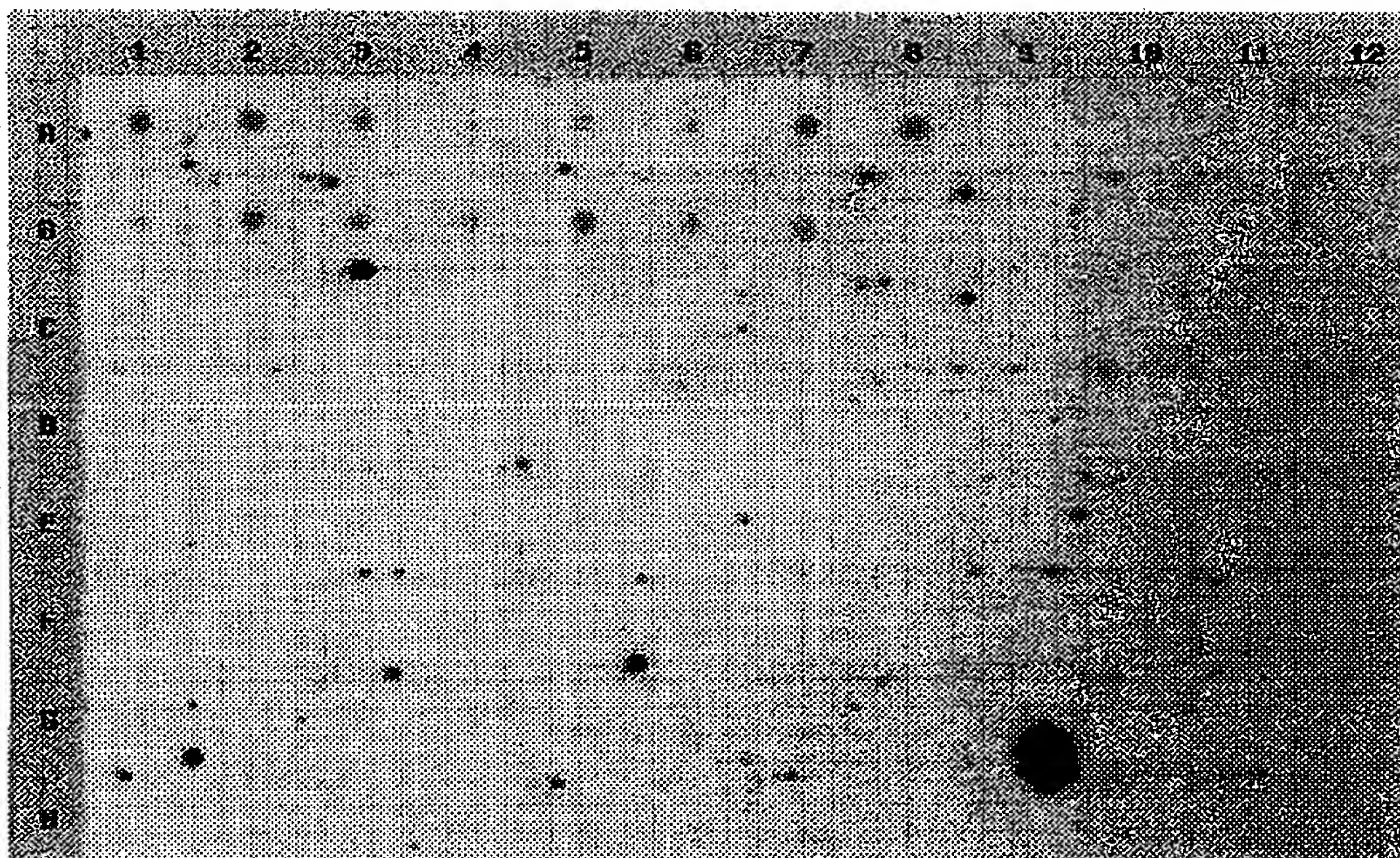


FIG. 2B

FIG. 5

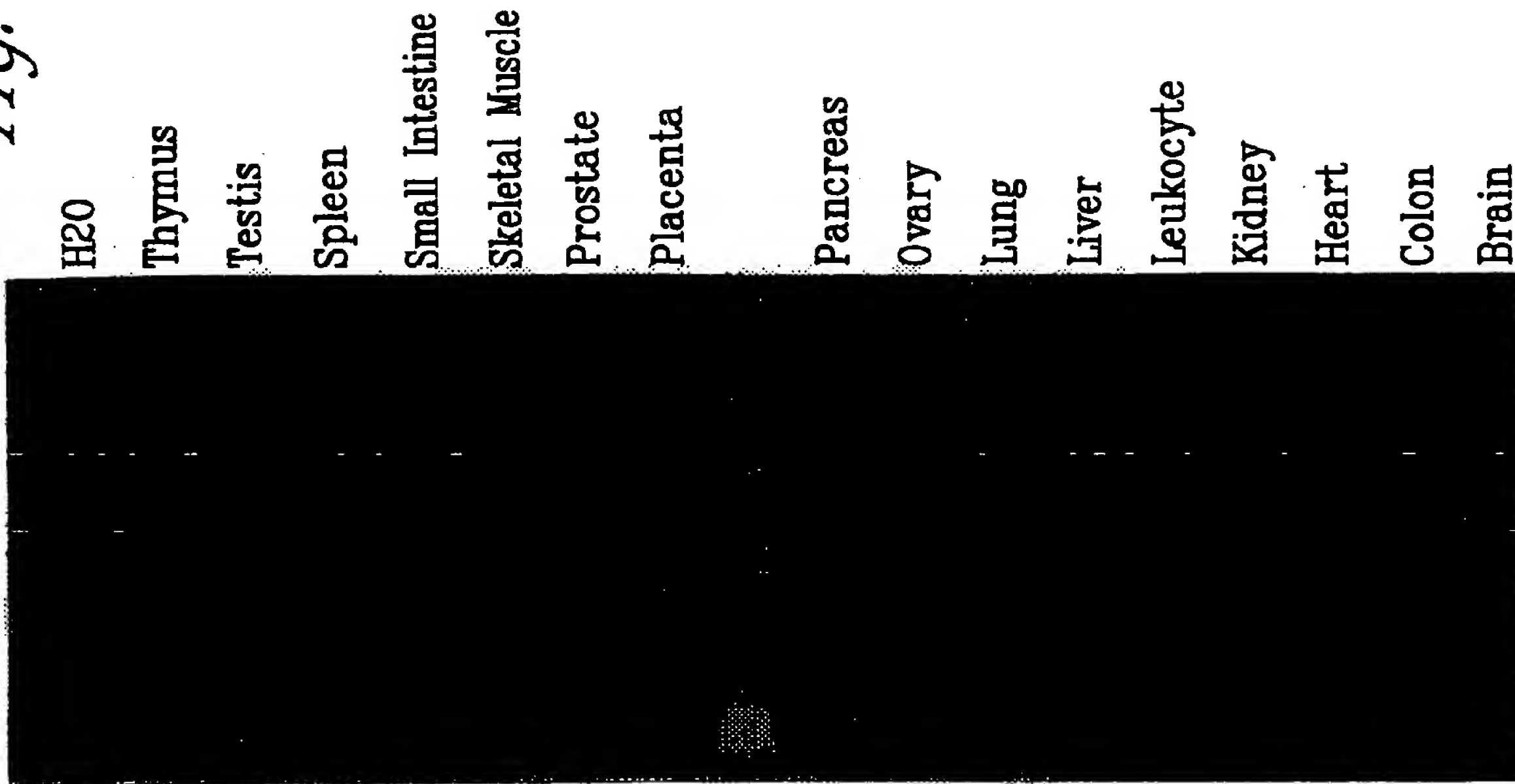


FIG. 4

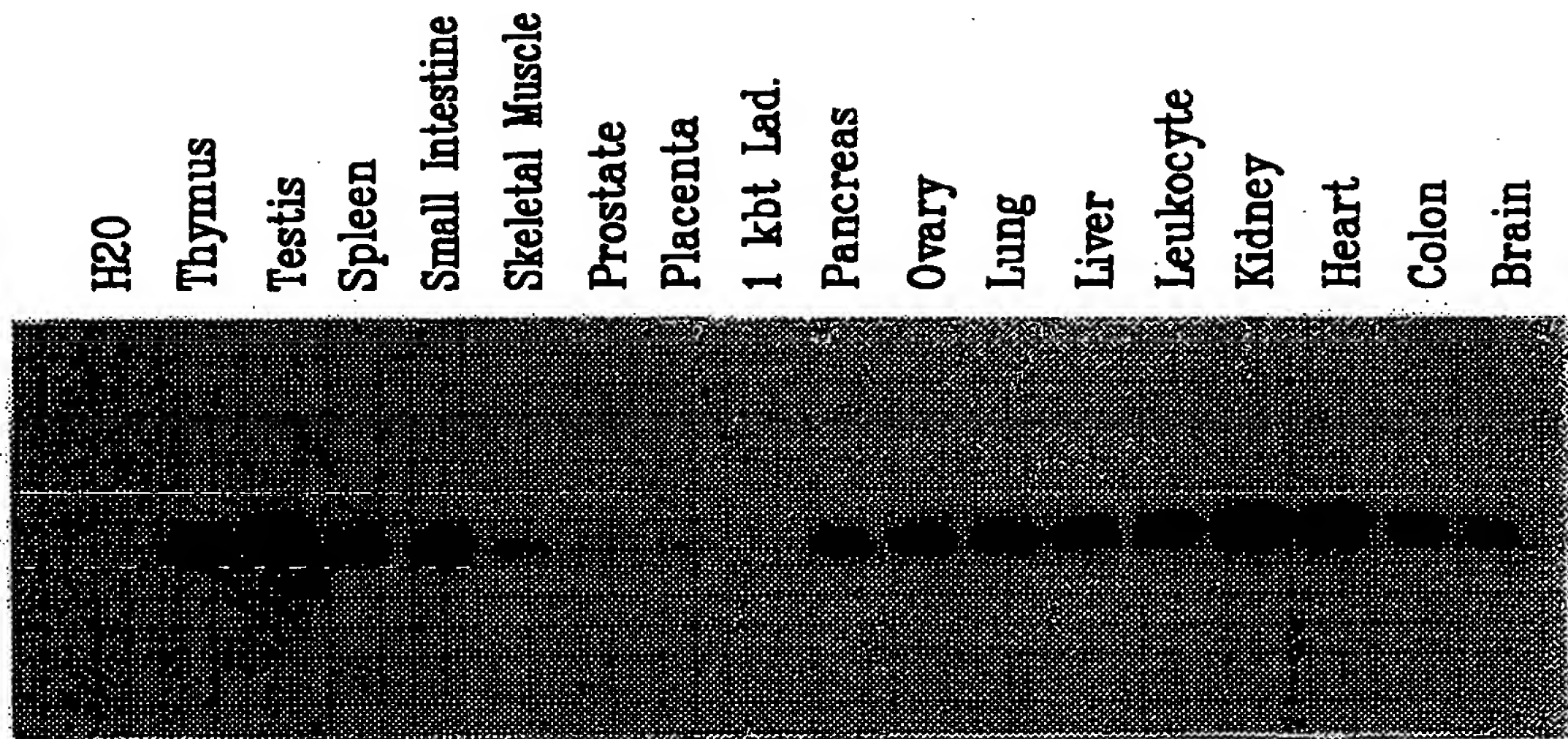
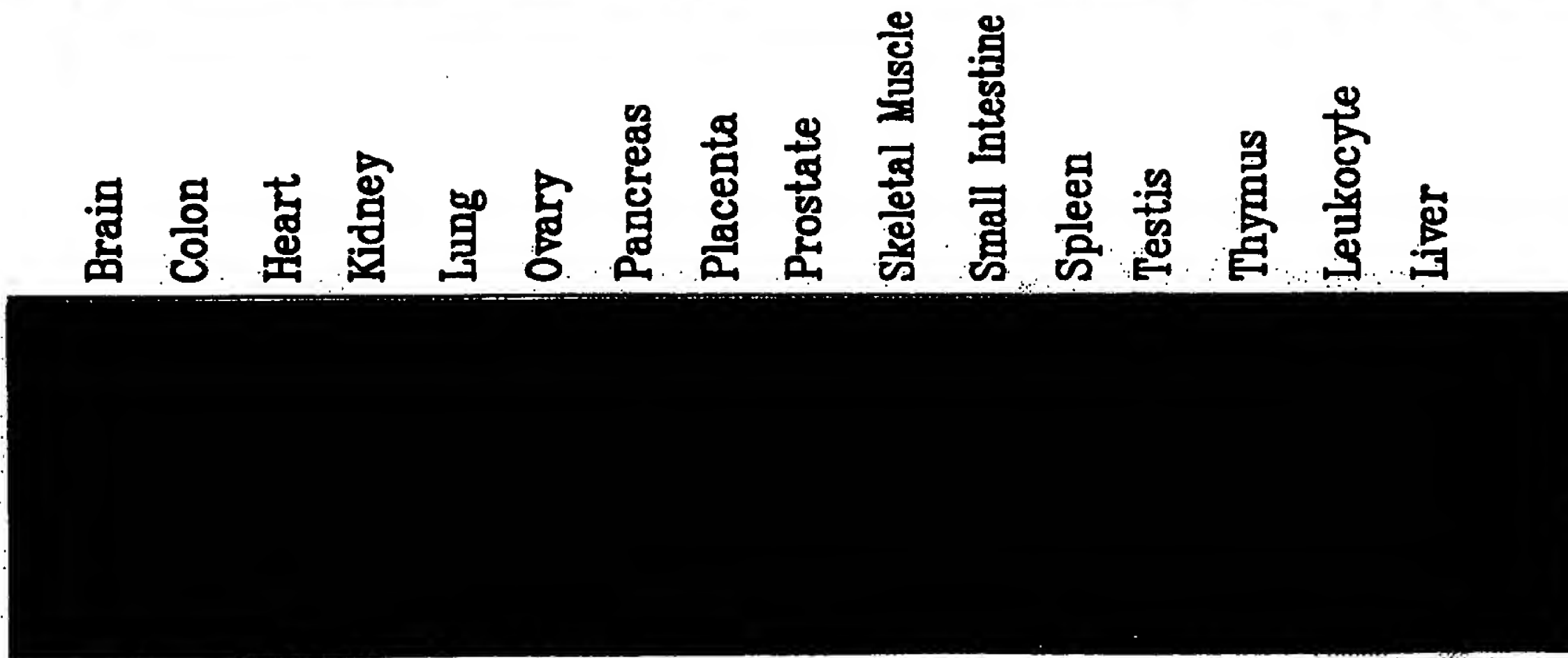


FIG. 3



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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chen, Ruoping
Dang, Huong T.
5 Liaw, Chen W.
Lin, I-Lin
- (ii) TITLE OF INVENTION: Human Orphan G Protein-Coupled Receptors
- (iii) NUMBER OF SEQUENCES: 74
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Arena Pharmaceuticals, Inc.
(B) STREET: 6166 Nancy Ridge Drive
(C) CITY: San Diego
(D) STATE: CA
15 (E) COUNTRY: USA
(F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
25 (C) CLASSIFICATION:
- ~~(viii) ATTORNEY/AGENT INFORMATION:~~
(A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787
- (ix) TELECOMMUNICATION INFORMATION:
30 (A) TELEPHONE: (858)453-7200
(B) TELEFAX: (858)453-7210

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1260 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

40 ATGGTCTTCT CGGCAGTGTT GACTGCGTTC CATACCGGGA CATCCAACAC AACATTTGTC 60

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GTGTATGAAA ACACCTACAT GAATATTACA CTCCCTCCAC CATTCCAGCA TCCTGACCTC 120
 AGTCCATTGC TTAGATATAG TTTTGAAACC ATGGCTCCCA CTGGTTTGAG TTCCTTGACC 180
 GTGAATAGTA CAGCTGTGCC CACAACACCA GCAGCATTTA AGAGCCTAAA CTTGCCTCTT 240
 CAGATCACCC TTTCTGCTAT AATGATATTC ATTCTGTTTG TGTCTTTTCT TGGGAACTTG 300
 5 GTTGTTTGCC TCATGGTTTA CCAAAAAGCT GCCATGAGGT CTGCAATTAA CATCCTCCTT 360
 GCCAGCCTAG CTTTTGCAGA CATGTTGCTT GCAGTGCTGA ACATGCCCTT TGCCCTGGTA 420
 ACTATTCTTA CTACCCGATG GATTTTTGGG AAATTCTTCT GTAGGGTATC TGCTATGTTT 480
 TTCTGGTTAT TTGTGATAGA AGGAGTAGCC ATCCTGCTCA TCATTAGCAT AGATAGGTTC 540
 CTTATTATAG TCCAGAGGCA GGATAAGCTA AACCCATATA GAGCTAAGGT TCTGATTGCA 600
 10 GTTTCTTGGG CAACTTCCTT TTGTGTAGCT TTTCCTTTAG CCGTAGGAAA CCCCAGCCTG 660
 CAGATACCTT CCCGAGCTCC CCAGTGTGTG TTTGGGTACA CAACCAATCC AGGCTACCAG 720
 GCTTATGTGA TTTTGATTTC TCTCATTCTT TTCTTCATAC CCTTCCTGGT AATACTGTAC 780
 TCATTTATGG GCATACTCAA CACCCTTCGG CACAATGCCT TGAGGATCCA TAGCTACCCT 840
 GAAGGTATAT GCCTCAGCCA GGCCAGCAAA CTGGGTCTCA TGAGTCTGCA GAGACCTTTC 900
 15 CAGATGAGCA TTGACATGGG CTTTAAAACA CGTGCCTTCA CCACTATTTT GATTCTCTTT 960
 GCTGTCTTCA TTGTCTGCTG GGCCCCATTC ACCACTTACA GCCTTGTGGC
 AACATTCACT1020

AAGCACTTTT ACTATCAGCA CAACTTTTTT GAGATTAGCA CCTGGCTACT GTGGCTCTGC1080
 TACCTCAAGT CTGCATTGAA TCCGCTGATC TACTACTGGA GGATTAAGAA ATTCCATGAT1140
 20 GCTTGCCTGG ACATGATGCC TAAGTCCTTC AAGTTTTTGC CGCAGCTCCC TGGTCACACA1200
 AAGCGACGGA TACGTCCTAG TGCTGTCTAT GTGTGTGGGG AACATCGGAC GGTGGTGTGA1260

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 419 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn
 1 5 10 15

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CTCTTCAGCG TGCCCTGGCT GGTCTTCCCC GAGGCTGCCG TCTGGTGGTA CGACCTGGTC 540
 ATCTGCCTGG ACTTCTGGGA CAGCGAGGAG CTGTCGCTGA GGATGCTGGA GGTCTTGGGG 600
 GGCTTCCTGC CTTTCCTCCT GCTGCTCGTC TGCCACGTGC TCACCCAGGC CACAGCCTGT 660
 CGCACCTGCC ACCGCCAACA GCAGCCCGCA GCCTGCCGGG GCTTCGCCCC TGTGGCCAGG 720
 5 ACCATTCTGT CAGCCTATGT GGTCTGAGG CTGCCCTACC AGCTGGCCCA GCTGCTCTAC 780
 CTGGCCTTCC TGTGGGACGT CTACTCTGGC TACCTGCTCT GGGAGGCCCT GGTCTACTCC 840
 GACTACCTGA TCCTACTCAA CAGCTGCCTC AGCCCCTTCC TCTGCCTCAT GGCCAGTGCC 900
 GACCTCCGGA CCCTGCTGCG CTCCTGCTC TCGTCCTTCG CGGCAGCTCT CTGCGAGGAG 960
 CGGCCGGGCA GCTTCACGCC CACTGAGCCA CAGACCCAGC TAGATTCTGA GGGTCCAAC1020
 10 CTGCCAGAGC CGATGGCAGA GGCCAGTCA CAGATGGATC CTGTGGCCCA GCCTCAGGTG1080
 AACCCACAC TCCAGCCACG ATCGGATCCC ACAGCTCAGC CACAGCTGAA CCCTACGGCC1140
 CAGCCACAGT CGGATCCCAC AGCCAGCCA CAGCTGAACC TCATGGCCCA GCCACAGTCA1200
 GATTCTGTGG CCCAGCCACA GGCAGACACT AACGTCCAGA CCCCTGCACC TGCTGCCAGT1260
 TCTGTGCCCA GTCCCTGTGA TGAAGCTTCC CCAACCCCAT CCTCGCATCC TACCCAGGG1320
 15 GCCCTTGAGG ACCCAGCCAC ACCTCCTGCC TCTGAAGGAG AAAGCCCCAG CAGCACCCCG1380
 CCAGAGGCGG CCCCGGGCGC AGGCCCCACG TGA 1413

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 468 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro
 1 5 10 15
 Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp
 20 25 30
 Thr Val Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro Ala Asn Gly
 30 35 40 45
 Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr

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	50	55	60
	Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe		
	65	70	75 80
5	Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His		
		85	90 95
	Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly		
		100	105 110
	Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp		
		115	120 125
10	Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro		
		130	135 140
	Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr		
		145	150 155 160
15	Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp		
		165	170 175
	Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser		
		180	185 190
	Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu		
		195	200 205
20	Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln		
		210	215 220
	Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile		
		225	230 235 240
25	Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu		
		245	250 255
	Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp		
		260	265 270
	Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu		
		275	280 285
30	Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu		
		290	295 300
	Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro		
		305	310 315 320
35	Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly		
		325	330 335
	Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro		
		340	345 350

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Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro
 355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro
 370 375 380

5 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser
 385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala
 405 410 415

10 Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser
 420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala
 435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly
 450 455 460

15 Ala Gly Pro Thr
 465

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25 ATGTCAGGGA TGGAAAACT TCAGAATGCT TCCTGGATCT ACCAGCAGAA ACTAGAAGAT 60
 CCATTCCAGA AACACCTGAA CAGCACCGAG GAGTATCTGG CCTTCCTCTG CGGACCTCGG 120
 CGCAGCCACT TCTTCCTCCC CGTGTCTGTG GTGTATGTGC CAATTTTGT GGTGGGGGTC 180
 ATTGGCAATG TCCTGGTGTG CCTGGTGATT CTGCAGCACC AGGCTATGAA GACGCCCACC 240
 AACTACTACC TCTTCAGCCT GCGGGTCTCT GACCTCCTGG TCCTGCTCCT TGGAAATGCCC 300
 30 CTGGAGGTCT ATGAGATGTG GCGCAACTAC CCTTTCTTGT TCGGGCCCGT GGGCTGCTAC 360
 TTCAAGACGG CCCTCTTTGA GACCGTGTGC TTCGCCTCCA TCCTCAGCAT CACCACCGTC 420
 AGCGTGGAGC GCTACGTGGC CATCCTACAC CCGTTCCGCG CCAAAGTCA GAGCACCCGG 480
 CGCCGGGCCC TCAGGATCCT CGGCATCGTC TGGGGCTTCT CCGTGCTCTT CTCCTGCCC 540

- 15 -

AACACCAGCA TCCATGGCAT CAAGTTCCAC TACTTCCCCA ATGGGTCCCT GGTCCCAGGT 600
 TCGGCCACCT GTACGGTCAT CAAGCCCATG TGGATCTACA ATTCATCAT CCAGGTCACC 660
 TCCTTCCTAT TCTACCTCCT CCCCATGACT GTCATCAGTG TCCTCTACTA CCTCATGGCA 720
 CTCAGACTAA AGAAAGACAA ATCTCTTGAG GCAGATGAAG GGAATGCAAA TATTCAAAGA 780
 5 CCCTGCAGAA AATCAGTCAA CAAGATGCTG TTTGTCTTGG TCTTAGTGTT TGCTATCTGT 840
 TGGGCCCCGT TCCACATTGA CCGACTCTTC TTCAGCTTTG TGGAGGAGTG GAGTGAATCC 900
 CTGGCTGCTG TGTTCAACCT CGTCCATGTG GTGTCAGGTG TCTTCTTCTA CCTGAGCTCA 960
 GCTGTCAACC CCATTATCTA TAACCTACTG TCTCGCCGCT TCCAGGCAGC ATTCCAGAAT1020
 GTGATCTCTT CTTTCCACAA ACAGTGGCAC TCCCAGCATG ACCCACAGTT GCCACCTGCC1080
 10 CAGCGGAACA TCTTCCTGAC AGAATGCCAC TTTGTGGAGC TGACCGAAGA TATAGGTCCC1140
 CAATTCCCAT GTCAGTCATC CATGCACAAC TCTCACCTCC CAACAGCCCT CTCTAGTGAA1200
 CAGATGTCAA GAACAAACTA TCAAAGCTTC CACTTTAACA AAACCTGA 1248

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 415 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln
 1 5 10 15
 Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
 20 25 30
 25 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
 35 40 45
 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
 50 55 60
 30 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
 65 70 75 80
 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
 85 90 95

- 16 -

	Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe	
	100	105 110
	Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr	
	115	120 125
5	Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg	
	130	135 140
	Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg	
	145	150 155 160
10	Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu	
	165	170 175
	Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe	
	180	185 190
	Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys	
	195	200 205
15	Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe	
	210	215 220
	Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala	
	225	230 235 240
20	Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala	
	245	250 255
	Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val	
	260	265 270
	Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg	
	275	280 285
25	Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val	
	290	295 300
	Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser	
	305	310 315 320
30	Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala	
	325	330 335
	Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln	
	340	345 350
	His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu	
	355	360 365
35	Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys	
	370	375 380
	Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu	
	385	390 395 400

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Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
 405 410 415

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCAGATA CTAATAGCAC AATCAATTTA TCACTAAGCA CTCGTGTTAC TTTAGCATTT 60
 TTTATGTCCT TAGTAGCTTT TGCTATAATG CTAGGAAATG CTTTGGTCAT TTTAGCTTTT 120
 GTGGTGGACA AAAACCTTAG ACATCGAAGT AGTTATTTTT TTCTTAACTT GGCCATCTCT 180
 GACTTCTTTG TGGGTGTGAT CTCCATTCCT TTGTACATCC CTCACACGCT GTTCGAATGG 240
 15 GATTTTGGAA AGGAAATCTG TGTATTTTGG CTCACTACTG ACTATCTGTT ATGTACAGCA 300
 TCTGTATATA ACATTGTCCT CATCAGCTAT GATCGATACC TGTCAGTCTC AAATGCTGTG 360
 TCTTATAGAA CTCAACATAC TGGGGTCTTG AAGATTGTTA CTCTGATGGT GGCCGTTTGG 420
 GTGCTGGCCT TCTTAGTGAA TGGGCCAATG ATTCTAGTTT CAGAGTCTTG GAAGGATGAA 480
 GGTAGTGAAT GTGAACCTGG ATTTTTTTTCG GAATGGTACA TCCTTGCCAT CACATCATTG 540
 20 TTGGAATTCG TGATCCCAGT CATCTTAGTC GCTTATTTC AATGAATAT TTATTGGAGC 600
 CTGTGGAAGC GTGATCATCT CAGTAGGTGC CAAAGCCATC CTGGACTGAC TGCTGTCTCT 660
 TCCAACATCT GTGGACACTC ATTCAGAGGT AGACTATCTT CAAGGAGATC TCTTTCTGCA 720
 TCGACAGAAG TTCCTGCATC CTTTCATTCA GAGAGACAGA GGAGAAAGAG TAGTCTCATG 780
 TTTTCCTCAA GAACCAAGAT GAATAGCAAT ACAATTGCTT CCAAATGGG TTCCTTCTCC 840
 25 CAATCAGATT CTGTAGCTCT TCACCAAAGG GAACATGTTG AACTGCTTAG AGCCAGGAGA 900
 TTAGCCAAGT CACTGGCCAT TCTCTTAGGG GTTTTTGCTG TTTGCTGGGC TCCATATTCT 960
 CTGTTCACAA TTGTCCTTTC ATTTTATTCC TCAGCAACAG GTCCTAAATC AGTTTGGTAT 1020
 AGAATTGCAT TTTGGCTTCA GTGGTTCAAT TCCTTTGTCA ATCCTCTTTT GTATCCATTG 1080
 TGTCACAAGC GCTTTCAAAA GGCTTTCTTG AAAATATTTT GTATAAAAAA GCAACCTCTA 1140
 30 CCATCACAAC ACAGTCGGTC AGTATCTTCT TAA 1173

- 18 -

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
 (B) TYPE: amino acid
 5 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10	Met	Pro	Asp	Thr	Asn	Ser	Thr	Ile	Asn	Leu	Ser	Leu	Ser	Thr	Arg	Val	1	5	10	15
	Thr	Leu	Ala	Phe	Phe	Met	Ser	Leu	Val	Ala	Phe	Ala	Ile	Met	Leu	Gly	20	25	30	
	Asn	Ala	Leu	Val	Ile	Leu	Ala	Phe	Val	Val	Asp	Lys	Asn	Leu	Arg	His	35	40	45	
15	Arg	Ser	Ser	Tyr	Phe	Phe	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Phe	Phe	Val	50	55	60	
	Gly	Val	Ile	Ser	Ile	Pro	Leu	Tyr	Ile	Pro	His	Thr	Leu	Phe	Glu	Trp	65	70	75	80
20	Asp	Phe	Gly	Lys	Glu	Ile	Cys	Val	Phe	Trp	Leu	Thr	Thr	Asp	Tyr	Leu	85	90	95	
	Leu	Cys	Thr	Ala	Ser	Val	Tyr	Asn	Ile	Val	Leu	Ile	Ser	Tyr	Asp	Arg	100	105	110	
	Tyr	Leu	Ser	Val	Ser	Asn	Ala	Val	Ser	Tyr	Arg	Thr	Gln	His	Thr	Gly	115	120	125	
25	Val	Leu	Lys	Ile	Val	Thr	Leu	Met	Val	Ala	Val	Trp	Val	Leu	Ala	Phe	130	135	140	
	Leu	Val	Asn	Gly	Pro	Met	Ile	Leu	Val	Ser	Glu	Ser	Trp	Lys	Asp	Glu	145	150	155	160
30	Gly	Ser	Glu	Cys	Glu	Pro	Gly	Phe	Phe	Ser	Glu	Trp	Tyr	Ile	Leu	Ala	165	170	175	
	Ile	Thr	Ser	Phe	Leu	Glu	Phe	Val	Ile	Pro	Val	Ile	Leu	Val	Ala	Tyr	180	185	190	
	Phe	Asn	Met	Asn	Ile	Tyr	Trp	Ser	Leu	Trp	Lys	Arg	Asp	His	Leu	Ser	195	200	205	
35	Arg	Cys	Gln	Ser	His	Pro	Gly	Leu	Thr	Ala	Val	Ser	Ser	Asn	Ile	Cys	210	215	220	

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Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala
 225 230 235 240
 Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys
 245 250 255
 5 Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile
 260 265 270
 Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His
 275 280 285
 10 Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser
 290 295 300
 Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser
 305 310 315 320
 Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys
 325 330 335
 15 Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe
 340 345 350
 Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala
 355 360 365
 20 Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His
 370 375 380
 Ser Arg Ser Val Ser Ser
 385 390

(16) INFORMATION FOR SEQ ID NO:15:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGCGAACG CGAGCGAGCC GGGTGGCAGC GGCGGCGGCG AGGCGGCCCGC CCTGGGCCTC 60
 AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTGCGG 120
 CTGCTGATCG TGCGGGAGCG CAGCCTGCAC CGCGCCCCGT ACTACCTGCT GCTCGACCTG 180
 TGCCTGGCCG ACGGGCTGCG CGCGCTCGCC TGCCTCCCGG CCGTCATGCT GGCGGCGCGG 240
 35 CGTGCGGCGG CCGCGGCGGG GGCGCCGCCG GGCGCGCTGG GCTGCAAGCT GCTCGCCTTC 300

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CTGGCCGCGC TCTTCTGCTT CCACGCCGCC TTCCTGCTGC TGGGCGTGGG CGTCACCCGC 360
TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCCGGCTG GCCGTGCGCC 420
GCCATGCTGG TGTGCGCCGC CTGGGCGCTG GCGCTGGCCG CGGCCTTCCC GCCAGTGCTG 480
GACGGCGGTG GCGACGACGA GGACGCGCCG TCGCCCTGG AGCAGCGGCC CGACGGCGCC 540
5 CCCGGCGCGC TGGGCTTCCT GCTGCTGCTG GCCGTGGTGG TGGGCGCCAC GCACCTCGTC 600
TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCCGCAAGA TCGGCCCCGC GCGCCTGGTG 660
CCCGCCGTCA GCCACGACTG GACCTTCCAC GGCCCGGGCG CCACCGGCCA GGCGGCCGCC 720
AACTGGACGG CGGGCTTCGG CCGCGGGCCC ACGCCGCCCG CGCTTGTTGG CATCCGGCCC 780
GCAGGGCCGG GCCGCGGCGC GCGCCGCCTC CTCGTGCTGG AAGAATTCAA GACGGAGAAG 840
10 AGGCTGTGCA AGATGTTCTA CGCCGTCACG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC 900
GTCGTGGCCA GCTACCTGCG GGTCTTGGTG CGGCCCGGCG CCGTCCCCCA GGCCTACCTG 960
ACGGCCTCCG TGTGGCTGAC CTTCGCGCAG GCCGGCATCA ACCCCGTCGT GTGCTTCCTC1020
TTCAACAGGG AGCTGAGGGA CTGCTTCAGG GCCCAGTTCC CCTGCTGCCA GAGCCCCCGG1080
ACCACCCAGG CGACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA 1128

15 (17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala
1 5 10 15
25 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser
20 25 30
Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser
35 40 45
30 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp
50 55 60
Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg
65 70 75 80

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu
100 105 110

5 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg
 115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val
130 135 140

10 Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu
145 150 155 160

Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg
165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val
180 185 190

15 Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile
195 200 205

His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser
210 215 220

	His	Asp	Trp	Thr	Phe	His	Gly	Pro	Gly	Ala	Thr	Gly	Gln	Ala	Ala	Ala
20	225					230					235					240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val
245 250 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val
260 265 270

25 Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala
 275 280 285

Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser
290 295 300

30 Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu
305 310 315 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val
325 330 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln
340 345 350

35 Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys
355 360 365

Asp Leu Lys Gly Ile Gly Leu

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370

375

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 ATGAACACCA CAGTGATGCA AGGCTTCAAC AGATCTGAGC GGTGCCCCAG AGACACTCGG 60
ATAGTACAGC TGGTATTCCC AGCCCTCTAC ACAGTGGTTT TCTTGACCGG CATCCTGCTG 120
AATACTTTGG CTCTGTGGGT GTTTGTTTAC ATCCCCAGCT CCTCCACCTT CATCATCTAC 180
CTCAAAAACA CTTTGGTGGC CGACTTGATA ATGACACTCA TGCTTCCTTT CAAAATCCTC 240
TCTGACTCAC ACCTGGCACC CTGGCAGCTC AGAGCTTTTG TGTGTCGTTT TTCTTCGGTG 300
15 ATATTTTATG AGACCATGTA TGTGGGCATC GTGCTGTTAG GGCTCATAGC CTTTGACAGA 360
TTCCTCAAGA TCATCAGACC TTTGAGAAAT ATTTTCTAA AAAAACCTGT TTTTGCAAAA 420
ACGGTCTCAA TCTTCATCTG GTTCTTTTTG TTCTTCATCT CCCTGCCAAA TACGATCTTG 480
AGCAACAAGG AAGCAACACC ATCGTCTGTG AAAAAGTGTG CTTCCTTAAA GGGGCCTCTG 540
GGGCTGAAAT GGCATCAAAT GGTAATAAC ATATGCCAGT TTATTTTCTG GACTGTTTTT 600
20 ATCCTAATGC TTGTGTTTTA TGTGGTTATT GCAAAAAAAG TATATGATTC TTATAGAAAG 660
TCCAAAAGTA AGGACAGAAA AAACAACAAA AAGCTGGAAG GCAAAGTATT TGTTGTCGTG 720
GCTGTCTTCT TTGTGTGTTT TGCTCCATTT CATTTTGCCA GAGTTCCATA TACTCACAGT 780
CAAACCAACA ATAAGACTGA CTGTAGACTG CAAAATCAAC TGTTTATTGC TAAAGAAACA 840
ACTCTCTTTT TGGCAGCAAC TAACATTTGT ATGGATCCCT TAATATACAT ATTCTTATGT 900
25 AAAAAATTCA CAGAAAAGCT ACCATGTATG CAAGGGAGAA AGACCACAGC ATCAAGCCAA 960
GAAAATCATA GCAGTCAGAC AGACAACATA ACCTTAGGCT GA 1002

(19) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

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(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

5	Met	Asn	Thr	Thr	Val	Met	Gln	Gly	Phe	Asn	Arg	Ser	Glu	Arg	Cys	Pro	1	5	10	15
	Arg	Asp	Thr	Arg	Ile	Val	Gln	Leu	Val	Phe	Pro	Ala	Leu	Tyr	Thr	Val	20	25	30	
	Val	Phe	Leu	Thr	Gly	Ile	Leu	Leu	Asn	Thr	Leu	Ala	Leu	Trp	Val	Phe	35	40	45	
10	Val	His	Ile	Pro	Ser	Ser	Ser	Thr	Phe	Ile	Ile	Tyr	Leu	Lys	Asn	Thr	50	55	60	
	Leu	Val	Ala	Asp	Leu	Ile	Met	Thr	Leu	Met	Leu	Pro	Phe	Lys	Ile	Leu	65	70	75	80
15	Ser	Asp	Ser	His	Leu	Ala	Pro	Trp	Gln	Leu	Arg	Ala	Phe	Val	Cys	Arg	85	90	95	
	Phe	Ser	Ser	Val	Ile	Phe	Tyr	Glu	Thr	Met	Tyr	Val	Gly	Ile	Val	Leu	100	105	110	
	Leu	Gly	Leu	Ile	Ala	Phe	Asp	Arg	Phe	Leu	Lys	Ile	Ile	Arg	Pro	Leu	115	120	125	
20	Arg	Asn	Ile	Phe	Leu	Lys	Lys	Pro	Val	Phe	Ala	Lys	Thr	Val	Ser	Ile	130	135	140	
	Phe	Ile	Trp	Phe	Phe	Leu	Phe	Phe	Ile	Ser	Leu	Pro	Asn	Thr	Ile	Leu	145	150	155	160
25	Ser	Asn	Lys	Glu	Ala	Thr	Pro	Ser	Ser	Val	Lys	Lys	Cys	Ala	Ser	Leu	165	170	175	
	Lys	Gly	Pro	Leu	Gly	Leu	Lys	Trp	His	Gln	Met	Val	Asn	Asn	Ile	Cys	180	185	190	
	Gln	Phe	Ile	Phe	Trp	Thr	Val	Phe	Ile	Leu	Met	Leu	Val	Phe	Tyr	Val	195	200	205	
30	Val	Ile	Ala	Lys	Lys	Val	Tyr	Asp	Ser	Tyr	Arg	Lys	Ser	Lys	Ser	Lys	210	215	220	
	Asp	Arg	Lys	Asn	Asn	Lys	Lys	Leu	Glu	Gly	Lys	Val	Phe	Val	Val	Val	225	230	235	240
35	Ala	Val	Phe	Phe	Val	Cys	Phe	Ala	Pro	Phe	His	Phe	Ala	Arg	Val	Pro	245	250	255	

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Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn
 260 265 270
 Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn
 275 280 285
 5 Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr
 290 295 300
 Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln
 305 310 315 320
 10 Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly
 325 330

(20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGGCCAACA CTACCGGAGA GCCTGAGGAG GTGAGCGGCG CTCTGTCCCC ACCGTCCGCA 60
 20 TCAGCTTATG TGAAGCTGGT ACTGCTGGGA CTGATTATGT GCGTGAGCCT GGCGGGTAAC 120
 GCCATCTTGT CCCTGCTGGT GCTCAAGGAG CGTGCCCTGC ACAAGGCTCC TTACTACTTC 180
 CTGCTGGACC TGTGCCTGGC CGATGGCATA CGCTCTGCCG TCTGCTTCCC CTTTGTGCTG 240
 GCTTCTGTGC GCCACGGCTC TTCATGGACC TTCAGTGCAC TCAGCTGCAA GATTGTGGCC 300
 TTTATGGCCG TGCTCTTTTG CTTCCATGCG GCCTTCATGC TGTTCATGCAT CAGCGTCACC 360
 25 CGCTACATGG CCATCGCCCA CCACCGCTTC TACGCCAAGC GCATGACACT CTGGACATGC 420
 GCGGCTGTCA TCTGCATGGC CTGGACCCTG TCTGTGGCCA TGGCCTTCCC ACCTGTCTTT 480
 GACGTGGGCA CCTACAAGTT TATTCGGGAG GAGGACCAGT GCATCTTTGA GCATCGCTAC 540
 TTCAAGGCCA ATGACACGCT GGGCTTCATG CTTATGTTGG CTGTGCTCAT GGCAGCTACC 600
 CATGCTGTCT ACGGCAAGCT GCTCCTCTTC GAGTATCGTC ACCGCAAGAT GAAGCCAGTG 660
 30 CAGATGGTGC CAGCCATCAG CCAGAACTGG ACATTCCATG GTCCCGGGGC CACCGGCCAG 720
 GCTGCTGCCA ACTGGATCGC CGGCTTTGGC CGTGGGCCCA TGCCACCAAC CCTGCTGGGT 780
 ATCCGGCAGA ATGGGCATGC AGCCAGCCGG CGGCTACTGG GCATGGACGA GGTC AAGGGT 840

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GAAAAGCAGC TGGGCCGCAT GTTCTACGCG ATCACACTGC TCTTTCTGCT CCTCTGGTCA 900
 CCCTACATCG TGGCCTGCTA CTGGCGAGTG TTTGTGAAAG CCTGTGCTGT GCCCCACCGC 960
 TACCTGGCCA CTGCTGTTTG GATGAGCTTC GCCCAGGCTG CCGTCAACCC AATTGTCTGC1020
 TTCCTGCTCA ACAAGGACCT CAAGAAGTGC CTGACCACTC ACGCCCCCTG CTGGGGCACA1080
 5 GGAGGTGCCC CGGCTCCCAG AGAACCCCTAC TGTGTCATGT GA 1122

(21) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

15	Met	Ala	Asn	Thr	Thr	Gly	Glu	Pro	Glu	Glu	Val	Ser	Gly	Ala	Leu	Ser	1	5	10	15
	Pro	Pro	Ser	Ala	Ser	Ala	Tyr	Val	Lys	Leu	Val	Leu	Leu	Gly	Leu	Ile	20	25	30	
	Met	Cys	Val	Ser	Leu	Ala	Gly	Asn	Ala	Ile	Leu	Ser	Leu	Leu	Val	Leu	35	40	45	
20	Lys	Glu	Arg	Ala	Leu	His	Lys	Ala	Pro	Tyr	Tyr	Phe	Leu	Leu	Asp	Leu	50	55	60	
	Cys	Leu	Ala	Asp	Gly	Ile	Arg	Ser	Ala	Val	Cys	Phe	Pro	Phe	Val	Leu	65	70	75	
25	Ala	Ser	Val	Arg	His	Gly	Ser	Ser	Trp	Thr	Phe	Ser	Ala	Leu	Ser	Cys	85	90	95	
	Lys	Ile	Val	Ala	Phe	Met	Ala	Val	Leu	Phe	Cys	Phe	His	Ala	Ala	Phe	100	105	110	
	Met	Leu	Phe	Cys	Ile	Ser	Val	Thr	Arg	Tyr	Met	Ala	Ile	Ala	His	His	115	120	125	
30	Arg	Phe	Tyr	Ala	Lys	Arg	Met	Thr	Leu	Trp	Thr	Cys	Ala	Ala	Val	Ile	130	135	140	
	Cys	Met	Ala	Trp	Thr	Leu	Ser	Val	Ala	Met	Ala	Phe	Pro	Pro	Val	Phe	145	150	155	
35	Asp	Val	Gly	Thr	Tyr	Lys	Phe	Ile	Arg	Glu	Glu	Asp	Gln	Cys	Ile	Phe	165	170	175	

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	Glu	His	Arg	Tyr	Phe	Lys	Ala	Asn	Asp	Thr	Leu	Gly	Phe	Met	Leu	Met	
				180					185					190			
	Leu	Ala	Val	Leu	Met	Ala	Ala	Thr	His	Ala	Val	Tyr	Gly	Lys	Leu	Leu	
			195					200					205				
5	Leu	Phe	Glu	Tyr	Arg	His	Arg	Lys	Met	Lys	Pro	Val	Gln	Met	Val	Pro	
		210					215					220					
	Ala	Ile	Ser	Gln	Asn	Trp	Thr	Phe	His	Gly	Pro	Gly	Ala	Thr	Gly	Gln	
	225					230					235					240	
10	Ala	Ala	Ala	Asn	Trp	Ile	Ala	Gly	Phe	Gly	Arg	Gly	Pro	Met	Pro	Pro	
				245						250					255		
	Thr	Leu	Leu	Gly	Ile	Arg	Gln	Asn	Gly	His	Ala	Ala	Ser	Arg	Arg	Leu	
				260					265					270			
	Leu	Gly	Met	Asp	Glu	Val	Lys	Gly	Glu	Lys	Gln	Leu	Gly	Arg	Met	Phe	
			275					280					285				
15	Tyr	Ala	Ile	Thr	Leu	Leu	Phe	Leu	Leu	Leu	Trp	Ser	Pro	Tyr	Ile	Val	
		290					295					300					
	Ala	Cys	Tyr	Trp	Arg	Val	Phe	Val	Lys	Ala	Cys	Ala	Val	Pro	His	Arg	
	305					310					315					320	
20	Tyr	Leu	Ala	Thr	Ala	Val	Trp	Met	Ser	Phe	Ala	Gln	Ala	Ala	Val	Asn	
					325					330					335		
	Pro	Ile	Val	Cys	Phe	Leu	Leu	Asn	Lys	Asp	Leu	Lys	Lys	Cys	Leu	Thr	
				340					345					350			
	Thr	His	Ala	Pro	Cys	Trp	Gly	Thr	Gly	Gly	Ala	Pro	Ala	Pro	Arg	Glu	
			355					360					365				
25	Pro	Tyr	Cys	Val	Met												
		370															

(22) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC 60

ACTTATGACT ACAGTCAATA TGAATTGATC TGTATCAAAG AAGATGTCAG AGAATTTGCA 120

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AAAGTTTTCC TCCCTGTATT CCTCACAATA GCTTTCGTCA TTGGACTTGC AGGCAATTCC 180
 ATGGTAGTGG CAATTTATGC CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC 240
 CTGAATTTGG CTGTAGCAGA TTTACTCCTT CTATTCCTC TGCCTTTTTG GGCTGTTAAT 300
 GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC CTTGTACACA 360
 5 CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGCATCA GCATAGACAG ATATGTGGCA 420
 GTAACATAATG TCCCCAGCCA ATCAGGAGTG GGAAAACCAT GCTGGATCAT CTGTTTCTGT 480
 GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC 540
 AATGCTAGGT GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT 600
 CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG GGTGTGCTAC 660
 10 TTTATCACGG CAAGGACACT CATGAAGATG CCAAACATTA AAATATCTCG ACCCCTAAAA 720
 GTTCTGCTCA CAGTCGTTAT AGTTTTCATT GTCACTCAAC TGCCTTATAA CATTGTCAAG 780
 TTCTGCCGAG CCATAGACAT CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC 840
 ATGGACATCG CCATCCAAGT CACAGAAAGC ATTGCACTCT TTCACAGCTG CCTCAACCCA 900
 ATCCTTTATG TTTTATGGG AGCATCTTTC AAAAAGTACG TTATGAAAGT GGCCAAGAAA 960
 15 TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT TTCCTTTTGA TTCTGAGGGT 1020
 CCTACAGAGC CAACCAGTAC TTTTAGCATT TAA 1053

(23) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
 1 5 10 15
 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
 20 25 30
 30 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
 35 40 45
 Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala

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	50		55		60											
	Ile	Tyr	Ala	Tyr	Tyr	Lys	Lys	Gln	Arg	Thr	Lys	Thr	Asp	Val	Tyr	Ile
	65					70					75				80	
5	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	Leu	Leu	Leu	Phe	Thr	Leu	Pro	Phe
					85					90					95	
	Trp	Ala	Val	Asn	Ala	Val	His	Gly	Trp	Val	Leu	Gly	Lys	Ile	Met	Cys
				100					105					110		
	Lys	Ile	Thr	Ser	Ala	Leu	Tyr	Thr	Leu	Asn	Phe	Val	Ser	Gly	Met	Gln
			115					120					125			
10	Phe	Leu	Ala	Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Val	Ala	Val	Thr	Asn	Val
	130						135					140				
	Pro	Ser	Gln	Ser	Gly	Val	Gly	Lys	Pro	Cys	Trp	Ile	Ile	Cys	Phe	Cys
	145					150					155					160
15	Val	Trp	Met	Ala	Ala	Ile	Leu	Leu	Ser	Ile	Pro	Gln	Leu	Val	Phe	Tyr
					165					170					175	
	Thr	Val	Asn	Asp	Asn	Ala	Arg	Cys	Ile	Pro	Ile	Phe	Pro	Arg	Tyr	Leu
				180					185					190		
	Gly	Thr	Ser	Met	Lys	Ala	Leu	Ile	Gln	Met	Leu	Glu	Ile	Cys	Ile	Gly
			195					200					205			
20	Phe	Val	Val	Pro	Phe	Leu	Ile	Met	Gly	Val	Cys	Tyr	Phe	Ile	Thr	Ala
	210						215					220				
	Arg	Thr	Leu	Met	Lys	Met	Pro	Asn	Ile	Lys	Ile	Ser	Arg	Pro	Leu	Lys
	225					230					235					240
25	Val	Leu	Leu	Thr	Val	Val	Ile	Val	Phe	Ile	Val	Thr	Gln	Leu	Pro	Tyr
					245					250					255	
	Asn	Ile	Val	Lys	Phe	Cys	Arg	Ala	Ile	Asp	Ile	Ile	Tyr	Ser	Leu	Ile
				260					265					270		
	Thr	Ser	Cys	Asn	Met	Ser	Lys	Arg	Met	Asp	Ile	Ala	Ile	Gln	Val	Thr
			275					280					285			
30	Glu	Ser	Ile	Ala	Leu	Phe	His	Ser	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Val
	290						295					300				
	Phe	Met	Gly	Ala	Ser	Phe	Lys	Asn	Tyr	Val	Met	Lys	Val	Ala	Lys	Lys
	305					310					315					320
35	Tyr	Gly	Ser	Trp	Arg	Arg	Gln	Arg	Gln	Ser	Val	Glu	Glu	Phe	Pro	Phe
					325					330					335	
	Asp	Ser	Glu	Gly	Pro	Thr	Glu	Pro	Thr	Ser	Thr	Phe	Ser	Ile		
				340					345					350		

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(24) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGCCAGGAA ACGCCACCCC AGTGACCACC ACTGCCCCGT GGGCCTCCCT GGGCCTCTCC 60
10 GCCAAGACCT GCAACAACGT GTCCTTCGAA GAGAGCAGGA TAGTCCTGGT CGTGGTGTAC 120
AGCGCGGTGT GCACGCTGGG GGTGCCGGCC AACTGCCTGA CTGCGTGGCT GGCCTGCTG 180
CAGGTACTGC AGGGCAACGT GCTGGCCGTC TACCTGCTCT GCCTGGCACT CTGCGAACTG 240
CTGTACACAG GCACGCTGCC ACTCTGGGTC ATCTATATCC GCAACCAGCA CCGCTGGACC 300
CTAGGCCTGC TGGCCTCGAA GGTGACCGCC TACATCTTCT TCTGCAACAT CTACGTCAGC 360
15 ATCCTCTTCC TGTGCTGCAT CTCCTGCGAC CGCTTCGTGG CCGTGGTGTA CGCGCTGGAG 420
AGTCGGGGCC GCCGCCGCCG GAGGACCGCC ATCCTCATCT CCGCCTGCAT CTTTCATCCTC 480
GTCCGGGATCG TTCCTACCC GGTGTTCCAG ACGGAAGACA AGGAGACCTG CTTTGACATG 540
CTGCAGATGG ACAGCAGGAT TGCCGGGTAC TACTACGCCA GGTTCACCGT TGGCTTTGCC 600
ATCCCTCTCT CCATCATCGC CTTACCAAC CACCGGATTT TCAGGAGCAT CAAGCAGAGC 660
20 ATGGGCTTAA GCGCTGCCCA GAAGGCCAAG GTGAAGCACT CGGCCATCGC GGTGGTTGTC 720
ATCTTCCTAG TCTGCTTCGC CCCGTACCAC CTGGTTCTCC TCGTCAAAGC CGCTGCCTTT 780
TCCTACTACA GAGGAGACAG GAACGCCATG TGCGGCTTGG AGGAAAGGCT GTACACAGCC 840
TCTGTGGTGT TTCTGTGCCT GTCCACGGTG AACGGCGTGG CTGACCCCAT TATCTACGTG 900
CTGGCCACGG ACCATTCCCG CCAAGAAGTG TCCAGAATCC ATAAGGGGTG GAAAGAGTGG 960
25 TCCATGAAGA CAGACGTCAC CAGGCTCACC CACAGCAGGG ACACCGAGGA GCTGCAGTCG1020
CCCGTGGCCC TTGCAGACCA CTACACCTTC TCCAGGCCCG TGCACCCACC AGGGTCACCA1080
TGCCCTGCAA AGAGGCTGAT TGAGGAGTCC TGCTGA 1116

(25) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 371 amino acids

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- (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Pro	Gly	Asn	Ala	Thr	Pro	Val	Thr	Thr	Thr	Ala	Pro	Trp	Ala	Ser	1	5	10	15
Leu	Gly	Leu	Ser	Ala	Lys	Thr	Cys	Asn	Asn	Val	Ser	Phe	Glu	Glu	Ser	20	25	30	
Arg	Ile	Val	Leu	Val	Val	Val	Tyr	Ser	Ala	Val	Cys	Thr	Leu	Gly	Val	35	40	45	
Pro	Ala	Asn	Cys	Leu	Thr	Ala	Trp	Leu	Ala	Leu	Leu	Gln	Val	Leu	Gln	50	55	60	
Gly	Asn	Val	Leu	Ala	Val	Tyr	Leu	Leu	Cys	Leu	Ala	Leu	Cys	Glu	Leu	65	70	75	80
Leu	Tyr	Thr	Gly	Thr	Leu	Pro	Leu	Trp	Val	Ile	Tyr	Ile	Arg	Asn	Gln	85	90	95	
His	Arg	Trp	Thr	Leu	Gly	Leu	Leu	Ala	Ser	Lys	Val	Thr	Ala	Tyr	Ile	100	105	110	
Phe	Phe	Cys	Asn	Ile	Tyr	Val	Ser	Ile	Leu	Phe	Leu	Cys	Cys	Ile	Ser	115	120	125	
Cys	Asp	Arg	Phe	Val	Ala	Val	Val	Tyr	Ala	Leu	Glu	Ser	Arg	Gly	Arg	130	135	140	
Arg	Arg	Arg	Arg	Thr	Ala	Ile	Leu	Ile	Ser	Ala	Cys	Ile	Phe	Ile	Leu	145	150	155	160
Val	Gly	Ile	Val	His	Tyr	Pro	Val	Phe	Gln	Thr	Glu	Asp	Lys	Glu	Thr	165	170	175	
Cys	Phe	Asp	Met	Leu	Gln	Met	Asp	Ser	Arg	Ile	Ala	Gly	Tyr	Tyr	Tyr	180	185	190	
Ala	Arg	Phe	Thr	Val	Gly	Phe	Ala	Ile	Pro	Leu	Ser	Ile	Ile	Ala	Phe	195	200	205	
Thr	Asn	His	Arg	Ile	Phe	Arg	Ser	Ile	Lys	Gln	Ser	Met	Gly	Leu	Ser	210	215	220	
Ala	Ala	Gln	Lys	Ala	Lys	Val	Lys	His	Ser	Ala	Ile	Ala	Val	Val	Val	225	230	235	240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys
245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly
260 265 270

5 Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser
 275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp
290 295 300

	His	Ser	Arg	Gln	Glu	Val	Ser	Arg	Ile	His	Lys	Gly	Trp	Lys	Glu	Trp
10	305					310					315					320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu
325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg
340 345 350

Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu
355 360 365

Glu Ser Cys
370

(26) INFORMATION FOR SEQ ID NO:25:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGCGAACT	ATAGCCATGC	AGCTGACAAC	ATTTTGCAA	ATCTCTCGCC	TCTAACAGCC	60
TTTCTGAAAC	TGACTTCCTT	GGGTTTCATA	ATAGGAGTCA	GCGTGGTGGG	CAACCTCCTG	120
ATCTCCATTT	TGCTAGTGAA	AGATAAGACC	TTGCATAGAG	CACCTTACTA	CTTCCTGTTG	180
30 GATCTTTGCT	GTTCAGATAT	CCTCAGATCT	GCAATTTGTT	TCCCATTTGT	GTTCAACTCT	240
GTCAAAAATG	GCTCTACCTG	GACTTATGGG	ACTCTGACTT	GCAAAGTGAT	TGCCTTTCTG	300
GGGGTTTTGT	CCTGTTTCCA	CACTGCTTTC	ATGCTCTTCT	GCATCAGTGT	CACCAGATAC	360
TTAGCTATCG	CCCATCACCG	CTTCTATACA	AAGAGGCTGA	CCTTTTGGAC	GTGTCTGGCT	420
GTGATCTGTA	TGGTGTGGAC	TCTGTCTGTG	GCCATGGCAT	TTCCCCCGGT	TTTAGACGTG	480

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GGCACTTACT CATTATTAG GGAGGAAGAT CAATGCACCT TCCAACACCG CTCCTTCAGG 540
 GCTAATGATT CCTTAGGATT TATGCTGCTT CTTGCTCTCA TCCTCCTAGC CACACAGCTT 600
 GTCTACCTCA AGCTGATATT TTTCGTCCAC GATCGAAGAA AAATGAAGCC AGTCCAGTTT 660
 GTAGCAGCAG TCAGCCAGAA CTGGACTTTT CATGGTCCTG GAGCCAGTGG CCAGGCAGCT 720
 5 GCCAATTGGC TAGCAGGATT TGGAAGGGGT CCCACACCAC CCACCTTGCT GGGCATCAGG 780
 CAAAATGCAA ACACCACAGG CAGAAGAAGG CTATTGGTCT TAGACGAGTT CAAAATGGAG 840
 AAAAGAATCA GCAGAATGTT CTATATAATG ACTTTTCTGT TTCTAACCTT GTGGGGCCCC 900
 TACCTGGTGG CCTGTTATTG GAGAGTTTTT GCAAGAGGGC CTGTAGTACC AGGGGGATTT 960
 CTAACAGCTG CTGTCTGGAT GAGTTTTGCC CAAGCAGGAA TCAATCCTTT TGTCTGCATT1020
 10 TTCTCAAACA GGGAGCTGAG GCGCTGTTTC AGCACAACCC TTCTTTACTG CAGAAAATCC1080
 AGGTTACCAA GGGAACCTTA CTGTGTTATA TGA 1113

(27) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20 Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
 1 5 10 15
 Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
 20 25 30
 25 Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
 35 40 45
 Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
 50 55 60
 Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
 65 70 75 80
 30 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
 85 90 95
 Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu

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	100	105	110
	Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe		
	115	120	125
5	Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met		
	130	135	140
	Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val		
	145	150	155 160
	Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His		
	165	170	175
10	Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala		
	180	185	190
	Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe		
	195	200	205
15	Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val		
	210	215	220
	Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala		
	225	230	235 240
	Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu		
	245	250	255
20	Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu		
	260	265	270
	Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr		
	275	280	285
25	Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala		
	290	295	300
	Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe		
	305	310	315 320
	Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro		
	325	330	335
30	Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr		
	340	345	350
	Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys		
	355	360	365
35	Val Ile		
	370		

(28) INFORMATION FOR SEQ ID NO:27:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGGTCC CGAACAGCAC CGGCCCGGAC AACGCGACGC TGCAGATGCT GCGGAACCCG 60
GCGATCGCGG TGGCCCTGCC CGTGGTGTAC TCGCTGGTGG CGGCGGTCAG CATCCCGGGC 120
10 AACCTCTTCT CTCTGTGGGT GCTGTGCCGG CGCATGGGGC CCAGATCCCC GTCGGTCATC 180
TTCATGATCA ACCTGAGCGT CACGGACCTG ATGCTGGCCA GCGTGTGACC TTTCCAAATC 240
TACTACCATT GCAACCGCCA CCACTGGGTA TTCGGGGTGC TGCTTTGCAA CGTGGTGACC 300
GTGGCCTTTT ACGCAAACAT GTATTCCAGC ATCCTCACCA TGACCTGTAT CAGCGTGGAG 360
CGCTTCCTGG GGGTCCTGTA CCCGCTCAGC TCCAAGCGCT GGCGCCGCCG TCGTTACGCG 420
15 GTGGCCGCGT GTGCAGGGAC CTGGCTGCTG CTCCTGACCG CCCTGTGCCC GCTGGCGCGC 480
ACCGATCTCA CCTACCCGGT GCACGCCCTG GGCATCATCA CCTGCTTCGA CGTCCTCAAG 540
TGGACGATGC TCCCCAGCGT GGCCATGTGG GCCGTGTTCC TCTTCACCAT CTTTCATCCTG 600
CTGTTCTCTA TCCCGTTCGT GATCACCGTG GCTTGTTACA CGGCCACCAT CCTCAAGCTG 660
TTGCGCACGG AGGAGGCGCA CGGCCGGGAG CAGCGGAGGC GCGCGGTGGG CCTGGCCGCG 720
20 GTGGTCTTGC TGGCCTTTGT CACCTGCTTC GCCCCAACA ACTTCGTGCT CCTGGCGCAC 780
ATCGTGAGCC GCCTGTTCTA CGGCAAGAGC TACTACCACG TGTACAAGCT CACGCTGTGT 840
CTCAGCTGCC TCAACAACCTG TCTGGACCCG TTTGTTTATT ACTTTGCGTC CCGGGAATTC 900
CAGCTGCGCC TGCGGGAATA TTTGGGCTGC CGCCGGGTGC CCAGAGACAC CCTGGACACG 960
CGCCGCGAGA GCCTCTTCTC CGCCAGGACC ACGTCCGTGC GCTCCGAGGC CGGTGCGCAC 1020
25 CCTGAAGGGA TGGAGGGAGC CACCAGGCCG GGCCTCCAGA GGCAGGAGAG TGTGTTCTGA 1080

(29) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
30 (C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

	Met	Gln	Val	Pro	Asn	Ser	Thr	Gly	Pro	Asp	Asn	Ala	Thr	Leu	Gln	Met	
	1				5					10					15		
5	Leu	Arg	Asn	Pro	Ala	Ile	Ala	Val	Ala	Leu	Pro	Val	Val	Tyr	Ser	Leu	
				20					25					30			
	Val	Ala	Ala	Val	Ser	Ile	Pro	Gly	Asn	Leu	Phe	Ser	Leu	Trp	Val	Leu	
			35					40					45				
10	Cys	Arg	Arg	Met	Gly	Pro	Arg	Ser	Pro	Ser	Val	Ile	Phe	Met	Ile	Asn	
	50						55					60					
	Leu	Ser	Val	Thr	Asp	Leu	Met	Leu	Ala	Ser	Val	Leu	Pro	Phe	Gln	Ile	
	65					70					75				80		
	Tyr	Tyr	His	Cys	Asn	Arg	His	His	Trp	Val	Phe	Gly	Val	Leu	Leu	Cys	
					85					90					95		
15	Asn	Val	Val	Thr	Val	Ala	Phe	Tyr	Ala	Asn	Met	Tyr	Ser	Ser	Ile	Leu	
				100					105					110			
	Thr	Met	Thr	Cys	Ile	Ser	Val	Glu	Arg	Phe	Leu	Gly	Val	Leu	Tyr	Pro	
				115				120					125				
20	Leu	Ser	Ser	Lys	Arg	Trp	Arg	Arg	Arg	Arg	Tyr	Ala	Val	Ala	Ala	Cys	
	130					135						140					
	Ala	Gly	Thr	Trp	Leu	Leu	Leu	Leu	Thr	Ala	Leu	Cys	Pro	Leu	Ala	Arg	
	145				150						155				160		
	Thr	Asp	Leu	Thr	Tyr	Pro	Val	His	Ala	Leu	Gly	Ile	Ile	Thr	Cys	Phe	
					165					170					175		
25	Asp	Val	Leu	Lys	Trp	Thr	Met	Leu	Pro	Ser	Val	Ala	Met	Trp	Ala	Val	
				180				185						190			
	Phe	Leu	Phe	Thr	Ile	Phe	Ile	Leu	Leu	Phe	Leu	Ile	Pro	Phe	Val	Ile	
			195					200					205				
30	Thr	Val	Ala	Cys	Tyr	Thr	Ala	Thr	Ile	Leu	Lys	Leu	Leu	Arg	Thr	Glu	
	210					215						220					
	Glu	Ala	His	Gly	Arg	Glu	Gln	Arg	Arg	Arg	Ala	Val	Gly	Leu	Ala	Ala	
	225				230						235				240		
	Val	Val	Leu	Leu	Ala	Phe	Val	Thr	Cys	Phe	Ala	Pro	Asn	Asn	Phe	Val	
				245						250				255			
35	Leu	Leu	Ala	His	Ile	Val	Ser	Arg	Leu	Phe	Tyr	Gly	Lys	Ser	Tyr	Tyr	
			260					265						270			

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His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
 275 280 285
 Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
 290 295 300
 5 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
 305 310 315 320
 Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
 325 330 335
 10 Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350
 Gln Arg Gln Glu Ser Val Phe
 355

(30) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGAGCGTC CCTGGGAGGA CAGCCCAGGC CCGGAGGGGG CAGCTGAGGG CTCGCCTGTG 60
 .CCAGTCGCCG CCGGGGCGCG CTCCGGTGCC GCGGCGAGTG GCACAGGCTG GCAGCCATGG 120
 GCTGAGTGCC CGGGACCCAA GGGGAGGGGG CAACTGCTGG CGACCGCCGG CCCTTTGCGT 180
 CGCTGGCCCG CCCCTCGCC TGCCAGCTCC AGCCCCGCCC CCGGAGCGGC GTCCGCTCAC 240
 25 TCGGTTCAAG GCAGCGCGAC TGCGGGTGGC GCACGACCAG GGC GCAGACC TTGGGGCGCG 300
 CGGCCCCATGG AGTCGGGGCT GCTGCGGCCG GCGCCGGTGA GCGAGGTCAT CGTCCTGCAT 360
 TACAACTACA CCGGCAAGCT CCGCGGTGCG AGCTACCAGC CGGGTGCCGG CCTGCGCGCC 420
 GACGCCGTGG TGTGCCTGGC GGTGTGCGCC TTCATCGTGC TAGAGAATCT AGCCGTGTTG 480
 TTGGTGCTCG GACGCCACCC GCGCTTCCAC GCTCCCATGT TCCTGCTCCT GGGCAGCCTC 540
 30 ACGTTGTGCG ATCTGCTGGC AGGCGCCGCC TACGCCGCCA ACATCCTACT GTCGGGGCCG 600
 CTCACGCTGA AACTGTCCCC CGCGCTCTGG TTCGCACGGG AGGGAGGCGT CTTCGTGGCA 660
 CTCACTGCGT CCGTGCTGAG CCTCCTGGCC ATCGCGCTGG AGCGCAGCCT CACCATGGCG 720

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CGCAGGGGGC CCGCGCCCGT CTCCAGTCGG GGGCGCACGC TGGCGATGGC AGCCGCGGCC 780
 TGGGGCGTGT CGCTGCTCCT CGGGCTCCTG CCAGCGCTGG GCTGGAATTG CCTGGGTCGC 840
 CTGGACGCTT GCTCCACTGT CTTGCCGCTC TACGCCAAGG CCTACGTGCT CTTCTGCGTG 900
 CTCGCCTTCG TGGGCATCCT GGCCGCGATC TGTGCACTCT ACGCGCGCAT CTACTGCCAG 960
 5 GTACGCGCCA ACGCGCGGCG CCTGCCGGCA CGGCCCGGGA CTGCGGGGAC CACCTCGACC1020
 CGGGCGCGTC GCAAGCCGCG CTCTCTGGCC TTGCTGCGCA CGCTCAGCGT GGTGCTCCTG1080
 GCCTTTGTGG CATGTTGGGG CCCCTCTTC CTGCTGCTGT TGCTCGACGT GGCCTGCCCG1140
 GCGCGCACCT GTCCTGTACT CCTGCAGGCC GATCCCTTCC TGGGACTGGC CATGGCCAAC1200
 TCACTTCTGA ACCCCATCAT CTACACGCTC ACCAACCGCG ACCTGCGCCA CGCGCTCCTG1260
 10 CGCCTGGTCT GCTGCGGACG CCACTCCTGC GGCAGAGACC CGAGTGGCTC CCAGCAGTCG1320
 GCGAGCGCGG CTGAGGCTTC CGGGGGCCTG CGCCGCTGCC TGCCCCCGGG CCTTGATGGG1380
 AGCTTCAGCG GCTCGGAGCG CTCATCGCCC CAGCGCGACG GGCTGGACAC CAGCGGCTCC1440
 ACAGGCAGCC CCGGTGCACC CACAGCCGCC CGGACTCTGG TATCAGAACC GGCTGCAGAC1500
 TGA 1503

15 (31) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu
 1 5 10 15
 25 Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala
 20 25 30
 Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly
 35 40 45
 30 Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala
 50 55 60
 Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His
 65 70 75 80

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	Ser	Val	Gln	Gly	Ser	Ala	Thr	Ala	Gly	Gly	Ala	Arg	Pro	Gly	Arg	Arg	
					85					90					95		
	Pro	Trp	Gly	Ala	Arg	Pro	Met	Glu	Ser	Gly	Leu	Leu	Arg	Pro	Ala	Pro	
				100					105					110			
5	Val	Ser	Glu	Val	Ile	Val	Leu	His	Tyr	Asn	Tyr	Thr	Gly	Lys	Leu	Arg	
			115					120					125				
	Gly	Ala	Ser	Tyr	Gln	Pro	Gly	Ala	Gly	Leu	Arg	Ala	Asp	Ala	Val	Val	
			130				135					140					
10	Cys	Leu	Ala	Val	Cys	Ala	Phe	Ile	Val	Leu	Glu	Asn	Leu	Ala	Val	Leu	
	145					150					155					160	
	Leu	Val	Leu	Gly	Arg	His	Pro	Arg	Phe	His	Ala	Pro	Met	Phe	Leu	Leu	
					165					170					175		
	Leu	Gly	Ser	Leu	Thr	Leu	Ser	Asp	Leu	Leu	Ala	Gly	Ala	Ala	Tyr	Ala	
				180					185					190			
15	Ala	Asn	Ile	Leu	Leu	Ser	Gly	Pro	Leu	Thr	Leu	Lys	Leu	Ser	Pro	Ala	
			195				200						205				
	Leu	Trp	Phe	Ala	Arg	Glu	Gly	Gly	Val	Phe	Val	Ala	Leu	Thr	Ala	Ser	
		210					215					220					
20	Val	Leu	Ser	Leu	Leu	Ala	Ile	Ala	Leu	Glu	Arg	Ser	Leu	Thr	Met	Ala	
	225					230					235				240		
	Arg	Arg	Gly	Pro	Ala	Pro	Val	Ser	Ser	Arg	Gly	Arg	Thr	Leu	Ala	Met	
					245					250					255		
	Ala	Ala	Ala	Ala	Trp	Gly	Val	Ser	Leu	Leu	Leu	Gly	Leu	Leu	Pro	Ala	
				260					265					270			
25	Leu	Gly	Trp	Asn	Cys	Leu	Gly	Arg	Leu	Asp	Ala	Cys	Ser	Thr	Val	Leu	
			275					280					285				
	Pro	Leu	Tyr	Ala	Lys	Ala	Tyr	Val	Leu	Phe	Cys	Val	Leu	Ala	Phe	Val	
		290					295					300					
30	Gly	Ile	Leu	Ala	Ala	Ile	Cys	Ala	Leu	Tyr	Ala	Arg	Ile	Tyr	Cys	Gln	
	305					310					315				320		
	Val	Arg	Ala	Asn	Ala	Arg	Arg	Leu	Pro	Ala	Arg	Pro	Gly	Thr	Ala	Gly	
				325						330					335		
	Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Lys	Pro	Arg	Ser	Leu	Ala	Leu	Leu	
				340					345					350			
35	Arg	Thr	Leu	Ser	Val	Val	Leu	Leu	Ala	Phe	Val	Ala	Cys	Trp	Gly	Pro	
			355				360						365				
	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Asp	Val	Ala	Cys	Pro	Ala	Arg	Thr	Cys	

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	370		375		380
	Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn				
	385		390		395 400
5	Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg				
		405		410	415
	His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg				
		420		425	430
	Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly				
		435		440	445
10	Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly				
		450		455	460
	Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser				
		465		470	475 480
15	Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu				
		485		490	495
	Pro Ala Ala Asp				
		500			

(32) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCAAGCCG TCGACAATCT CACCTCTGCG CCTGGGAACA CCAGTCTGTG CACCAGAGAC 60

TACAAAATCA CCCAGGTCCT CTTCCCACTG CTCTACACTG TCCTGTTTTT TGTTGGACTT 120

ATCACAAATG GCCTGGCGAT GAGGATTTTC TTTCAAATCC GGAGTAAATC AAACCTTTATT 180

ATTTTTCTTA AGAACACAGT CATTTCTGAT CTTCTCATGA TTCTGACTTT TCCATTCAAA 240

30 ATTCTTAGTG ATGCCAAACT GGGAACAGGA CCACTGAGAA CTTTTGTGTG TCAAGTTACC 300

TCCGTCATAT TTTATTTTAC AATGTATATC AGTATTTTCT TCCTGGGACT GATAACTATC 360

GATCGCTACC AGAAGACCAC CAGGCCATTT AAAACATCCA ACCCCAAAAA TCTCTTGGGG 420

GCTAAGATTC TCTCTGTTGT CATCTGGGCA TTCATGTTCT TACTCTCTTT GCCTAACATG 480

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ATTCTGACCA ACAGGCAGCC GAGAGACAAG AATGTGAAGA AATGCTCTTT CCTTAAATCA 540
 GAGTTCGGTC TAGTCTGGCA TGAAATAGTA AATTACATCT GTCAAGTCAT TTTCTGGATT 600
 AATTTCTTAA TTGTTATTGT ATGTTATACA CTCATTACAA AAGAACTGTA CCGGTCATAC 660
 GTAAGAACGA GGGGTGTAGG TAAAGTCCCC AGGAAAAAGG TGAACGTCAA AGTTTTTCATT 720
 5 ATCATTGCTG TATTCTTTAT TTGTTTTGTT CCTTTCCATT TTGCCCCGAAT TCCTTACACC 780
 CTGAGCCAAA CCCGGGATGT CTTTGACTGC ACTGCTGAAA ATACTCTGTT CTATGTGAAA 840
 GAGAGCACTC TGTGGTTAAC TTCCTTAAAT GCATGCCTGG ATCCGTTTCAT CTATTTTTTTC 900
 CTTTGCAAGT CCTTCAGAAA TTCCTTGATA AGTATGCTGA AGTGCCCCAA TTCTGCAACA 960
 TCTCTGTCCC AGGACAATAG GAAAAAAGAA CAGGATGGTG GTGACCCAAA TGAAGAGACT1020
 10 CCAATGTAA 1029

(33) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 15 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant.

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

20 Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
 1 5 10 15
 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
 20 25 30
 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
 35 40 45
 25 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
 50 55 60
 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
 65 70 75 80
 30 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
 85 90 95
 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
 100 105 110
 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg

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	115	120	125
	Pro Phe Lys Thr Ser Asn	Pro Lys Asn Leu Leu	Gly Ala Lys Ile Leu
	130	135	140
5	Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met	145	150 155 160
	Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser	165	170 175
	Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr	180	185 190
10	Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys	195	200 205
	Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg	210	215 220
15	Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile	225	230 235 240
	Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg	245	250 255
	Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala	260	265 270
20	Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser	275	280 285
	Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser	290	295 300
25	Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr	305	310 315 320
	Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro	325	330 335
	Asn Glu Glu Thr Pro Met	340	

30 (34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA GACTTCGCGG 60
 GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG GGCTGCCTGG CAACGGCTTC 120
 GTGGTGTGGA GCTTGGCGGG CTGGCGGCCT GCACGGGGGC GACCGCTGGC GGCCACGCTT 180
 5 GTGCTGCACC TGGCGCTGGC CGACGGCGCG GTGCTGCTGC TCACGCCGCT CTTTGTGGCC 240
 TTCCTGACCC GGCAGGCCTG GCCGCTGGGC CAGGCGGGCT GCAAGGCGGT GTACTACGTG 300
 TGC GCGCTCA GCATGTACGC CAGCGTGCTG CTCACCGGCC TGCTCAGCCT GCAGCGCTGC 360
 CTCGCAGTCA CCCGCCCTT CCTGGCGCCT CGGCTGCGCA GCCCGGCCCT GGCCCGCCGC 420
 CTGCTGCTGG CGGTCTGGCT GGCCGCCCTG TTGCTCGCCG TCCCGGCCGC CGTCTACCGC 480
 10 CACCTGTGGA GGGACCGCGT ATGCCAGCTG TGCCACCCGT CGCCGGTCCA CGCCGCCGCC 540
 CACCTGAGCC TGGAGACTCT GACCGCTTTC GTGCTTCCTT TCGGGCTGAT GCTCGGCTGC 600
 TACAGCGTGA CGCTGGCAGC GCTGCGGGGC GCCCGCTGGG GCTCCGGGCG GCACGGGGCG 660
 CGGGTGGGCC GGCTGGTGAG CGCCATCGTG CTTGCCTTCG GCTTGCTCTG GGCCCCCTAC 720
 CACGCAGTCA ACCTTCTGCA GGCGGTCGCA GCGCTGGCTC CACCGGAAGG GGCCTTGGCG 780
 15 AAGCTGGGCG GAGCCGGCCA GGCGGCGCGA GCGGGAATA CGGCCTTGGC CTTCTTCAGT 840
 TCTAGCGTCA ACCCGGTGCT CTACGTCTTC ACCGCTGGAG ATCTGCTGCC CCGGGCAGGT 900
 CCCCGTTTCC TCACGCGGCT CTTTGAAGGC TCTGGGGAGG CCCGAGGGGG CGGCCGCTCT 960
 AGGGAAGGGA CCATGGAGCT CCGAACTACC CCTCAGCTGA AAGTGGTGGG GCAGGGCCGC 1020
 GGCAATGGAG ACCCGGGGGG TGGGATGGAG AAGGACGGTC CGGAATGGGA CCTTTGA 1077

20 (35) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp
 1 5 10 15
 30 Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu

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	20	25	30
	Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp		
	35	40	45
5	Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu		
	50	55	60
	Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala		
	65	70	75 80
	Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala		
		85	90 95
10	Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr		
		100	105 110
	Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu		
		115	120 125
15	Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala		
		130	135 140
	Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg		
		145	150 155 160
	His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val		
		165	170 175
20	His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu		
		180	185 190
	Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu		
		195	200 205
25	Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg		
		210	215 220
	Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr		
		225	230 235 240
	His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu		
		245	250 255
30	Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly		
		260	265 270
	Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr		
		275	280 285
35	Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu		
		290	295 300
	Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser		
		305	310 315 320

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Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val
 325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp
 340 345 350

5 Gly Pro Glu Trp Asp Leu
 355

(36) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1005 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

15 ATGCTGGGGA TCATGGCATG GAATGCAACT TGCAAAACT GGCTGGCAGC AGAGGCTGCC 60
 CTGGAAAAGT ACTACCTTTC CATTTTTTAT GGGATTGAGT TCGTTGTGGG AGTCCTTGGA 120
 AATACCATTG TTGTTTACGG CTACATCTTC TCTCTGAAGA ACTGGAACAG CAGTAATATT 180
 TATCTCTTTA ACCTCTCTGT CTCTGACTTA GCTTTTCTGT GCACCCTCCC CATGCTGATA 240
 AGGAGTTATG CCAATGGAAA CTGGATATAT GGAGACGTGC TCTGCATAAG CAACCGATAT 300
 20 GTGCTTCATG CCAACCTCTA TACCAGCATT CTCTTTCTCA CTTTATCAG CATAGATCGA 360
 TACTTGATAA TTAAGTATCC TTTCCGAGAA CACCTTCTGC AAAAGAAAGA GTTTGCTATT 420
 TTAATCTCCT TGGCCATTTG GGTTTTAGTA ACCTTAGAGT TACTACCCAT ACTTCCCCTT 480
 ATAAATCCTG TTATAACTGA CAATGGCACC ACCTGTAATG ATTTTGCAAG TTCTGGAGAC 540
 CCCAACTACA ACCTCATTTA CAGCATGTGT CTAACACTGT TGGGGTTCCT TATTCCTCTT 600
 25 TTTGTGATGT GTTTCTTTTA TTACAAGATT GCTCTCTTCC TAAAGCAGAG GAATAGGCAG 660
 GTTGCTACTG CTCTGCCCCT TGAAAAGCCT CTCAACTTGG TCATCATGGC AGTGGTAATC 720
 TTCTCTGTGC TTTTACACC CTATCACGTC ATGCGGAATG TGAGGATCGC TTCACGCCTG 780
 GGGAGTTGGA AGCAGTATCA GTGCACTCAG GTCGTCATCA ACTCCTTTTA CATTGTGACA 840
 CGGCCTTTGG CCTTCTGAA CAGTGTCATC AACCTGTCT TCTATTTTCT TTTGGGAGAT 900
 30 CACTTCAGGG ACATGCTGAT GAATCAACTG AGACACAACT TCAAATCCCT TACATCCTTT 960
 AGCAGATGGG CTCATGAACT CCTACTTTCA TTCAGAGAAA AGTGA 1005

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(37) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

10	Met	Leu	Gly	Ile	Met	Ala	Trp	Asn	Ala	Thr	Cys	Lys	Asn	Trp	Leu	Ala	1	5	10	15
	Ala	Glu	Ala	Ala	Leu	Glu	Lys	Tyr	Tyr	Leu	Ser	Ile	Phe	Tyr	Gly	Ile	20	25	30	
	Glu	Phe	Val	Val	Gly	Val	Leu	Gly	Asn	Thr	Ile	Val	Val	Tyr	Gly	Tyr	35	40	45	
15	Ile	Phe	Ser	Leu	Lys	Asn	Trp	Asn	Ser	Ser	Asn	Ile	Tyr	Leu	Phe	Asn	50	55	60	
	Leu	Ser	Val	Ser	Asp	Leu	Ala	Phe	Leu	Cys	Thr	Leu	Pro	Met	Leu	Ile	65	70	75	80
20	Arg	Ser	Tyr	Ala	Asn	Gly	Asn	Trp	Ile	Tyr	Gly	Asp	Val	Leu	Cys	Ile	85	90	95	
	Ser	Asn	Arg	Tyr	Val	Leu	His	Ala	Asn	Leu	Tyr	Thr	Ser	Ile	Leu	Phe	100	105	110	
	Leu	Thr	Phe	Ile	Ser	Ile	Asp	Arg	Tyr	Leu	Ile	Ile	Lys	Tyr	Pro	Phe	115	120	125	
25	Arg	Glu	His	Leu	Leu	Gln	Lys	Lys	Glu	Phe	Ala	Ile	Leu	Ile	Ser	Leu	130	135	140	
	Ala	Ile	Trp	Val	Leu	Val	Thr	Leu	Glu	Leu	Leu	Pro	Ile	Leu	Pro	Leu	145	150	155	160
30	Ile	Asn	Pro	Val	Ile	Thr	Asp	Asn	Gly	Thr	Thr	Cys	Asn	Asp	Phe	Ala	165	170	175	
	Ser	Ser	Gly	Asp	Pro	Asn	Tyr	Asn	Leu	Ile	Tyr	Ser	Met	Cys	Leu	Thr	180	185	190	
	Leu	Leu	Gly	Phe	Leu	Ile	Pro	Leu	Phe	Val	Met	Cys	Phe	Phe	Tyr	Tyr	195	200	205	
35	Lys	Ile	Ala	Leu	Phe	Leu	Lys	Gln	Arg	Asn	Arg	Gln	Val	Ala	Thr	Ala	210	215	220	

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Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile
 225 230 235 240
 Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile
 245 250 255
 5 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val
 260 265 270
 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser
 275 280 285
 10 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp
 290 295 300
 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe
 305 310 315 320
 Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys
 325 330

15 (38) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGCAGGCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAACCTG 60
 ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG 120
 25 CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC 180
 TTTGGCAATG CTCTGGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC 240
 AACATCTTTA TCTGCTCCTT GCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC 300
 GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG 360
 GTGCCATTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT 420
 30 GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTAAAATGA AGTGGCAATA CACCAACCGA 480
 AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG 540
 TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC 600
 TGCTTAGAAG AGTGGACCAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC 660

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ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA 720
 CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA 780
 ATGTCCAAAA TAGCCAGGAA GAAGAAACGA GCTGTCATTA TGATGGTGAC AGTGGTGGCT 840
 CTCTTTGCTG TGTGCTGGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT 900
 5 TTTGAAAAGG AATATGATGA TGTCAACAATC AAGATGATTT TTGCTATCGT GCAAATTATT 960
 GGATTTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACCTTCAA1020
 AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA1080
 AGGCATGGAA ATTCAGGAAT TACAATGATG CGGAAGAAAG CAAAGTTTTT CCTCAGAGAG1140
 AATCCAGTGG AGGAAACCAA AGGAGAAGCA TTCAGTGATG GCAACATTGA AGTCAAATTG1200
 10 TGTGAACAGA CAGAGGAGAA GAAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA1260
 CTGGCTGAGA ATTCTCCTTT AGACAGTGGG CATTAA 1296

(39) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 431 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
 1 5 10 15
 Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
 20 25 30
 25 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
 35 40 45
 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
 50 55 60
 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
 65 70 75 80
 30 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
 85 90 95
 Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu

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	100	105	110
	Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala		
	115	120	125
5	Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His		
	130	135	140
	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg		
	145	150	155
	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val		
	165	170	175
10	Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe		
	180	185	190
	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro		
	195	200	205
15	Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu		
	210	215	220
	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu		
	225	230	235
	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile		
	245	250	255
20	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val		
	260	265	270
	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro		
	275	280	285
25	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu		
	290	295	300
	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile		
	305	310	315
	Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn		
	325	330	335
30	Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val		
	340	345	350
	Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr		
	355	360	365
35	Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu		
	370	375	380
	Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu		
	385	390	395
			400

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Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
 405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
 420 425 430

5 (40) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTGTGTACAG CAGTTCGCAG AGTG

24

(41) INFORMATION FOR SEQ ID NO:40:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGTGCCAGG CAGAGCAGGT AGAC

24

(42) INFORMATION FOR SEQ ID NO:41:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGAATTCC TGCTTGCTCC CAGCTTGGCC C

31

(43) INFORMATION FOR SEQ ID NO:42:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGTGGATCCT GCTGTCAAAG GTCCCATTCG GG

32

10 (44) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCACAATGCT AGGTGTGGTC

20

20 (45) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGCATAGACA ATGGGATTAC AG

22

30 (46) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACAATGCT AGGTGTGGTC TGGCTGGTGG CAGTCATCGT AGGATCACCC ATGTGGCACG 60
5 TGCAACAAC TGAATCAAA TATGACTTCC TATATGAAAA GGAACACATC TGCTGCTTAG 120
AAGAGTGGAC CAGCCCTGTG CACCAGAAGA TCTACACCAC CTTTCATCCTT GTCATCCTCT 180
TCCTCCTGCC TCTTATGGTG ATGCTTATTC TGTACGTAAA ATTGGTTATG AACTTTGGAT 240
AAAGAAAAGA GTTGGGGATG GTTCAGTGCT TCGAACTATT CATGGAAAAG AAATGTCCAA 300
AATAGCCAGG AAGAAGAAAC GAGCTGTCAT TATGATGGTG ACAGTGGTGG CTCTCTTTGC 360
10 TGTGTGCTGG GCACCATTCC ATGTTGTCCA TATGATGATT GAATACAGTA ATTTTGAAAA 420
GGAATATGAT GATGTCACAA TCAAGATGAT TTTTGCTATC GTGCAAATTA TTGGATTTTC 480
CAACTCCATC TGTAATCCCA TTGTCTATGC A 511

(47) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGCTTAGAA GAGTGGACCA G 21

(48) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTGTGCACCA GAAGATCTAC AC

22

(49) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAAGGATGAA GGTGGTGTAG A

21

(50) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTGTAGATCT TCTGGTGCAC AGG

23

(51) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAATGCAGG TCATAGTGAG C

21

(52) INFORMATION FOR SEQ ID NO:51:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
- 10 TGGAGCATGG TGACGGGAAT GCAGAAG 27
- (53) INFORMATION FOR SEQ ID NO:52:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
- 20 GTGATGAGCA GGTCAGTGG CGCCAAG 27
- (54) INFORMATION FOR SEQ ID NO:53:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
- 30 GCAATGCAGG CGCTTAACAT TAC 23
- (55) INFORMATION FOR SEQ ID NO:54:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTGGGTTACA ATCTGAAGGG CA

22

(56) INFORMATION FOR SEQ ID NO:55:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACTCCGTGTC CAGCAGGACT CTG

23

(57) INFORMATION FOR SEQ ID NO:56:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TGCGTGTTCC TGGACCCTCA CGTG

24

(58) INFORMATION FOR SEQ ID NO:57:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 55 -

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CAGGCCTTGG ATTTTAATGT CAGGGATGG

29

5 (59) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGAGAGTCAG CTCTGAAAGA ATTCAGG

27

15 (60) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGATGTGATG CCAGATACTA ATAGCAC

27

25 (61) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

- 56 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCTGATTCAT TTAGGTGAGA TTGAGAC

27

(62) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACAGGTACC TTGCCATCAA G

21

(63) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGCACAATG CCAGTGATAA GG

22

(64) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGACTTCTT GTTCCTGGCA GCAGCGG

27

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(65) INFORMATION FOR SEQ ID NO:64:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

10 AGACCAGCCA GGGCACGCTG AAGAGTG

27

(66) INFORMATION FOR SEQ ID NO:65:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

20 GATCAAGCTT CCATCCTACT GAAACCATGG TC

32

(67) INFORMATION FOR SEQ ID NO:66:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

30 GATCAGATCT CAGTTCCAAT ATTACACCA CCGTC

35

(68) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGGTGTGCT CCATGGCATC CC

22

(69) INFORMATION FOR SEQ ID NO:68:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTAAGCCTCC CAGAACGAGA GG

22

(70) INFORMATION FOR SEQ ID NO:69:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGCGCAGGG TGAAGCCTGA GAGC

24

(71) INFORMATION FOR SEQ ID NO:70:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- 59 -

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGCACCTGCT GTGACCTGTG CAGG

24

5 (72) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTCCTGCCAC TTCGAGACAT GG

22

15 (73) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAAACTTCTC TGCCCTTACC GTC

23

25 (74) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCAACACCAG CATCCATGGC ATCAAG

26

(75) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGAGAGTCAG CTCTGAAAGA ATTCAGG

27